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extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, new varieties of flowering plants. Other contemplated uses include, in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                         81.9%; Score 68; DB 5; Length 16;
87.5%; Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mason J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-terminal amino acid sequence of a CFM #11.
                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                              colour-facilitating molecule (CFM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB99071 standard; peptide; 16 AA.
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21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002; 2002WO-GB000928.
                                                                                                                                                                                                                                                                                                                                          1 SVIAKOMTYKVYMSGT 16
                                                                                                                                                                                                                                                                                                                                                                        SVIATOMTYKVYMPGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                            14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-740765/80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoegh-Guldberg IO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UV sink; sunscreen.
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JONES E L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200270703-A2.
                                                                                                                                                                                                                                              Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB99071;
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                                                                                                                                                                                                                                                                                                              Matches
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous

Claim 4; Page 281; 510pp; English.

white light.

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transgenic animal which exhibits a novel colour e.g. sheep with blue or transgenic animal which exhibits a novel colour e.g. sheep with blue or cred coloured fleece. They are useful for producing coloured blant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of upholstery. CFMs modify visible colour in edible and/or ornamental in sunscreens. CFMs modify visible colour in edible and/or ornamental clugal species, and in fruits and vegetables to enhance their situations of distorted light specira (Dhomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                             Score 67; DB 5; Lengtn 10, Pred. No. 2.88-05;
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Prescott M;
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                                                                                                                                                                                                                                                               colour-facilitating molecule (CFM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB99069 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                         0;
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21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
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                                                                                                                                                                                                                                                                                                                             80.7%;
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                                                                                                                                                                                                                                                                                                                                                                                              1 SVIAKOMTYKVYMSGT
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Best Local Similarity 87.5
Matches 14; Conservative
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(UYQU ) UNIV QUEENSLAND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-740765/80
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(JONE/) JONES E L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UV sink; sunscreen
                                                                                                                                                                                                                                                                                                Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB99069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB99069
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comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CPMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or coloured flaece. They are useful for producing coloured plant certactors, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional coloured transducing or intensifying an image, providing additional coloured to growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, carpression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental carporter in species and in fruits and vegetables to enhance their carbonates. CFMs modify visible colour improve image quality in situations of distorted light species (dromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a
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Sequence 16 AA;

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79.5%; Score 66; DB 5; Length 16; 87.5%; Pred. No. 4.3e-05; ive 0; Mismatches 2; Indels
                                                                          1 SVIAKOMTYKVYMSGT 16
                                                                                                       1 SGIATOMTYKVYMSGT 16
Query Match
Best Local Similarity 87.5
Matches 14; Conservative
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Gaps

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N-terminal amino acid sequence of a CFM #14. ABB99074 standard; peptide; 16 AA. (first entry) UV sink; sunscreen. 22-JAN-2003 ABB99074; RESULT 10 ABB99074

Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; note= "Xaa is any amino acid except Val" note= "Xaa is any amino acid except Lys" Location/Qualifiers 'label= Xaa label= Xaa Misc-difference Misc-difference Misc-difference Unidentified

/note= "Xaa is any amino acid except Met" WO200270703-A2

12-SEP-2002.

label≈ Xaa

01-MAR-2002; 2002WO-GB000928 02-MAR-2001; 2001US-0273227P. 2001AU-00003874, 2001US-0329816P. (NUFA-) NUFARM LTD. (UYQU) UNIV QUEENSLAND. (JONE/) JONES E L. 21-MAR-2001; 15-OCT-2001;

The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous con-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or calculated fleece. They are useful for producing coloured plant cases include transducing or intensifying an image, providing agent. Other cuses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include. CFMs and offy visible colour in edible and/or ornamental cfungal species, and in fruits and vegetables to enhance their amental cfungal species, and in fruits and vegetables to enhance their contemplations of distorted light specira (bhomatrix). The first all-protein chromonhove in he isolated and markerial contemplated the contemplated the contemplated contemplate Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-Gaps chromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a .. 74.7%; Score 62; DB 5; Length 16; 81.2%; Pred. No. 0.00023; 1.1ve 0; Mismatches 3; Indels SG; Dove Mason J, Brugliera F, Prescott M; Claim 4; Page 282; 510pp; English. colour-facilitating molecule (CFM) Conservative WPI; 2002-740765/80 Hoegh-Guldberg 10, Local Similarity es 13; Conserv AA; white light Sequence 16 Query Match Matches

1 SVIAKOMIYKVYMSGT 16

16

SVIAKOMIYXXXXXSGT

à 셤 ABP70008 standard; peptide; 13 AA.

RESULT 11 ABP70008 ABP70008;

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Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; Colour Facilitating molecule (CFM) related sequence #SEQ ID 184. (revised)
(first entry) flower industry; ex UV sink; sunscreen. Pavona decussata. WO200270703-A2. 06-AUG-2003 22-JAN-2003

02-MAR-2001; 2001US-0273227P. 21-MAR-2001; 2001AU-00003874. 15-OCT-2001; 2001US-0329816P. 01-MAR-2002; 2002WO-GB000928. 12-SEP-2002

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The invention relates to an isolated colour-facilitating molecule (CFM)

comprising a polypeptide which, in a cell, alone or together with one or

comprising a polypeptide which, in a cell, alone or together with one or

content molecules imparts an altered characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

cranspenic animal which exhibits a novel colour e.g. sheep with blue or

cractoried fleece. They are useful for producing coloured plant

cractoried ransducing or intensifying an image, providing additional

clight for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics and car

conting materials that experience UV damage e.g. plastics and car

conting materials phototropic organisms e.g. algae and/or corals,

conting materials plants. Other contemplated uses include,

content of markers, general reporter molecules, photon traps, UV sinks or

content or markers, general reporter molecules, photon traps, UV sinks or

content or markers, general reporter molecules, photon traps, UV sinks or

content or markers and in fruits and vegetables to enhance their

chungal species and in fruits and vegetables to enhance their

chromophore to be isolated was Green Fluorescent protein (GFP). The

sequences given in records ABP69924-ABP70048 represent CFM related amino

caid sequences. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                               Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metalloprotease; enzyme; MP; p45; fusarium oxysporum; bacillus;
thermolysin; casein; Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 5; Length 13;
Pred. No. 10;
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                                                                                        Dove SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.4%; Scor.
100.0%; Pred. No. 10.
                                                                                  Brugliera F, Mason J, Prescott M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR77526 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                Claim 5; Page 473; 510pp; English.
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               NUFARM LTD.
UNIV QUEENSLAND.
JONES E L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
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                                                                                          Karan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                               WPI; 2002-740765/80
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                                                                                          Jones EL, Karan M,
Hoegh-Guldberg IO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVIAKOMT
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12-JUN-1996
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                                                                                                                                                                                                                                              white light.
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                 (NUFA-)
                                                       (JONE/)
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Gaps

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                                                                                                                                                                                                             metalloprotease (MP). This sequence represents the N-terminus of Fusarium metalloprotease (MP). This sequence represents the N-terminus of Fusarium coxysporum MP p45 (see AAR77528). AAR77525 represents the consensus N-terminal sequence of the MP from F.oxysporum and Aspergillus oryzae. P45 is a new MP, and has 10 times more efficiency than Bacillus MP. Bacillus MP is more effective in cleaving primary amino groups from casein. P45 has thermolysin-like activity, and is used to cleave a pro-sequence from a recombinant proenzyme to generate an active mature enzyme. The MP may be added to, or produced in, the broth where the proenzyme is being formed by a recombinant host cell converted with a vector containing the DNA encoding p45. The MP can also be used to assay the level of activatable proenzyme in a sample. (Updated on 25-MAR-2003 to correct PA
                                                                                                                          Fungal metallo:protease converts pro:enzyme to active form - has thermolysin-like activity, useful to cleave pro-sequence of pro:enzyme to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   öĘ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 2; Length 14; Pred. No. 2.2e+02; Mismatches 2; Indels
                                                                    Branner
                                                                    Fuglsang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusarium oxysporum; strain DSM 2672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW05846 standard; peptide; 14 AA.
                                                                      Madden M,
                                                                                                                                                                                       Claim 12; Page 36; 62pp; English.
                          (NOVO ) NOVO-NORDISK BIOTECH INC (NOVO ) NOVO-NORDISK AS.
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75.0%;
95US-00398489
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nes 6, Conservative
                                                                       Moyer DL,
                                                                                                                                                            generate mature enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TYKVYPWG 9
                                                                                                   WPI; 1995-404122/51
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14 AA;
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 03-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lehmbeck J;
                                                                       Shuster JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW05846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   field.
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Example 1; Page 34; 51pp; English

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AAW39598 standard; peptide; 11

(first entry)

11-JUN-1998

AAW39598;

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AAW39598
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             The N-terminal sequence (AAM05846) of Fusarium oxysporum DSM 2672 p45 metalloprotease (see also AAW05845) was identified by amino acid analysis of a protein isolated from a fermentation broth. A PCR primer based on this peptide was used, together with a primer based as a p45 internal peptide, in the PCR cloning of the p45 gene (AAT40131) from F. oxysporum genomic DNA. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zinc finger protein 53. The sequences can be used in the treatment of cancer, haemopathy, nervous system disorders, development disorders, metabolic disorders, inflammation, immunological diseases and HIV infection. The present sequence is the N-terminus of the protein of the
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide-human zinc finger protein 53 and polynucleotide for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; zinc finger protein 53; cancer; nervous system disease; development disorder; metabolic disease; inflammation; haemopathy; immunological disease; HIV infection; gene therapy.
                                                                                                                                                                                                 0;
                                                                                                                                                                Score 29; DB 2; Length 14;
Pred. No. 2.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.9%; Score 29; DB 5; Length 15; 54.5%; Pred. No. 2.3e+02; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human zinc finger protein 53 N-terminal peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BODE-) BODE GENE DEV CO LTD SHANGHAI
                                                                                                                                                                                                                                                                                                                                     AAM48968 standard; peptide; 15 AA.
                                                                                                                                                          Query Match 34.9%;
Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                            Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                     AAM48968;
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AAM48968
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immunogenic T-cell peptide epitopes present in polypeptide antigens. The method involves the identification of peptide sequences capable of binding to an HLA (human leukocyte antigen) class I molecule and measuring the binding of this epitope peptide to the HLA class I peptide. The stability of binding of the peptide and WHC (major histocompatability complex) class I molecule is measured on intact human B cells carrying the MHC molecule at their cell surfaces. The method can be used to select peptide epitopes for generating vaccines against a disease associated peptide epitopes for generating vaccines against a disease associated with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral immune responses. Peptide AMM3558 is derived from the human melanome associated protein tyrosinase which is capable of upregulating HLA-A*0201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides AAW39430-W39734 are used in a novel method for the selection of
                                                                                                                                            ij.
                                                                                                                                 T cell epitope; immune response; human leukocyte antigen; HLA Class : vaccine; immunogenic; major histocompatablilty complex; MHC; B cell; disease; anti-tumour; anti-viral.
                                                                                                     Human melanoma associated protein tyrosinase peptide (pos. 367-377).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method of selecting T cell peptide epitope(s) - by measuring stability of HLA class I-peptide complexes on intact B cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 2; Le
Pred. No. 2.5e+02;
3; Mismatches 0;
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecules on T2 cells
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Best Local Similarity
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5 KQMTYKVYMSG 15 KNMTLKSFASG 12

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Sequence 4, Appli Sequence 22, Appl Sequence 253, App Sequence 48, Appl Sequence 2392, Ap Sequence 34, Appl Sequence 11, Appl

Appli , Appl

Sequence 5, # Sequence 38,

1 US-10-416-822-4 1 US-10-416-822-4 1 US-09-92-93-253 2 US-09-93-253 4 US-10-762-629-48 1 US-09-754-831A-34 1 US-09-812-5-57A-2292 1 US-10-388-33-11 US-09-812-528-5 US-09-812-528-5 US-09-812-528-5 US-09-812-83-11 US-09-812-83-13 US-09-812-83-13 US-09-812-83-13 US-09-812-83-13 US-09-812-83-13 US-09-812-127 US-09-818-121-27 US-09-818-121-27 US-09-818-121-27 US-09-818-121-27 US-09-818-121-27 US-09-818-121-27 US-09-818-121-27 US-09-818-121-27 US-09-818-121-27 US-09-918-460-60

31.3 31.3 31.3 31.3 31.3 30.1

Sequence 38, Sequence 21, Sequence 13, Sequence 27, 1

Sequence 21, Appl Sequence 23, Appl Sequence 28, Appl Sequence 33, Appl Sequence 30, Appl Sequence 37, Appl Sequence 77, Appl Sequence 19, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 14, Appl Sequence 145, Appl

US-09-898-860-32 US-09-077-439A-7 US-10-213-286-519 US-09-77-805-112 US-09-77-805-112 US-09-77-805-112 US-10-289-566-1 US-10-289-566-1 US-10-367-594-145 US-10-367-594-145 US-10-367-654-145 US-10-367-654-145 US-10-367-654-145 US-10-367-658-145 US-10-367-658-145 US-10-367-658-145

Sequence 28, Al Sequence 33, Al Sequence 60, Al Sequence 32,

145, App 60, Appl

Sequence Sequence

US-09-872-836-60

ALIGNMENTS

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August 12, 2004, 07:04:56; Search time 41 Seconds (without alignments) 130.165 Million cell updates/sec
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Sequence 492,
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1: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-253-286-493
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US-10-253-286-508
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                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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  Sequence 187, Application US/10360101
Publication No. US20040009550A1
GENERAL INFORMATION:
APPLICANT: Woll, Gert N.
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way FILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: EP 02077060.8
PRIOR APPLICATION NUMBER: EP 02077060.8
NUMBER OF SEQ ID NOS: 309
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 187
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Publication No. US20040058881A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
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US-10-253-286-492
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US-10-360-101-187
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NUMBER OF SEQ ID NOS: 905
SOFTWARRE: Patentin Ver. 2.1
SEQ ID NO 492
LENGTH: 9
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1 IYMNGTM 7
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US-10-245-871-493
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US-10-253-266-493
US-10-253-266-493
Sequence 493, Application US/10253286
Publication No. US20040058881A1
GENERAL INFORMATION:
APPLICANT: HUMPHEREY, ROBERT
APPLICANT: HUMPHEREY, ROBERT
TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2015
CURRENT APPLICATION NUMBER: 10/197,000
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
           TITLE OF INVENTION: I1-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES FILE REFERENCE: REH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER: OF SEQ ID NOS: 905
SOFTWARE: Patentin Ver: 2.1
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CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
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Pred. No. 1.2e+06;
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57.1%;
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                         TYPE: PRT
, ORGANISM: Homo sapiens
US-10-253-286-492
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ORGANISM: Homo sapiens
XU, MINZHEN
                                                                                                                                                                                                                                                                                                                                                                                              11 VYMSGTV 17
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Matches 4; Conserv
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1 IYMNGTM 7
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GENERAL INFORMATION:
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| Publication No. US20030235594A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: HUMPHREYS, ROBERT
| APPLICANT: HUMPHREYS, ROBERT
| TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| TILE REFERENCE: REH-2013
| CURRENT APPLICATION NUMBER: 10/197,000
| PRIOR PILING DATE: 2002-07-17
| PRIOR PILING DATE: 1999-09-14
| NUMBER OF SEQ ID NOS: 905
| SOFTWARE: PALCHIN VET. 2.1
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Publication No. US2040058881A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: HUMPHREYS, ROBERT
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT APPLICATION NUMBER: 10/197,000
PRIOR PRILING DATE: 2002-07-17
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SEQ ID NO 508
LUMPHREY PATENTING US SOUTH NOW SEQ ID NOS: 905
SEQ ID NO 508
LUMPHREY PATENTING LATER SALENTING LATER S
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PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Ii-key/tyrosinase overlapping hybrid peptide
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                                                                                                                                                                                                               33.7%; Score 28; DB 15; Length 9; 57.1%; Pred. No. 1.2e+06;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-492
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Gaps

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Length 14; 0; Indels

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OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Ii-key/tyrosinase overlapping hybrid peptide
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Pred. No. 2.7e+02;
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OTHER INFORMATION: a-aminovaleric acid
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NAME/KEX: MOD RES
LOCATION: (5)
OTHER INFORMATION: a-aminovaleric acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 509, Application US/10245871
Publication No. US20030235594A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: C-term amidated US-10-245-871-509
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                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                       Query Match 33.7%;
Best Local Similarity 57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 509
NUMBER OF SEQ ID NOS: 905
SOFTWARE: Patentin Ver. 2.1
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6 IYMNGTM 12
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8 IYMNGTM 14
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Matches 4; Conserv
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US-10-253-286-501
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                                         SEQ ID NO 508
                                                               LENGTH: 14
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TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2012

CURRENT APPLICATION NUMBER: US/10/253,286

CURRENT FILING DATE: 2003-01-13

PRIOR PLICATION NUMBER: 10/197,000

PRIOR PLICATION NUMBER: 10/197,000

PRIOR PLICATION NUMBER: 09/396,813

PRIOR PLING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 905

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 509

LENGTH: 14

TYPE: PRI

ORGANISM: Artificial Sequence
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Publication No. US20030235594A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
TITLE OF INVENTION: 11. KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR APPLICATION NUMBER: 0/197,000
PRIOR APPLICATION NUMBER: 0/396,813
PRIOR FILING DATE: 1999-09-14
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57.1%; Pred. No. 2.7e+02;
tive 3; Mismatches 0.
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                   NAME/KEY: MOD_RES
LOCATION: (5)
OTHER INFORMATION: a-aminovaleric acid
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 509, Application US/10253286; Publication No. US20040058881A1; GENERAL INFORMATION: APPLICANT: HUMPHREYS, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: C-term amidated US-10-253-286-509
                                                                                ; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-253-286-508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 VYMSGTV 17
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8 IYMNGTM 14
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6 IYMNGTM 12
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NAME/KEY: MOD_RES
LOCATION: (5)
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APPLICANT: HUMPHREYS, ROBERT
APPLICANT: WU MINZHEN
TITLE CANT: WU MINZHEN
TITLE OF INVENTION: 11. KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REPRENCE: REH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT PILING DATE: 2003-01-09
PRIOR FILING DATE: 2002-07-17
PRIOR FILING DATE: 10/197,000
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Ii-key/tyrosinase overlapping hybrid peptide
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| Sequence 510, Application US/10245871
| Publication No. US20030235594A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: HUMPHREYS, ROBERT
| APPLICANT: KU, MINZHEN
| TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| FILE REFERENCE: REH-2013
| CURRENT APPLICATION NUMBER: 10/10/245,871
| PRIOR FILING DATE: 2003-01-09
| PRIOR APPLICATION NUMBER: 10/197,000
| PRIOR PELICATION NUMBER: 09/396,813
| PRIOR FILING DATE: 1999-09-14
| PRIOR PELICATION NUMBER: 09/396,813
| NUMBER OF SEQ ID NOS: 905
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 510
                   TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES FILE REFERENCE: REH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PATENTIN Ver. 2.1
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Pred. No. 3.4e+02;
3; Mismatches 0; Indels
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GENERAL INFORMATION: ABPLICANT: DeGroot, Anne S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-245-871-510
                                                                                                                                                                                                                                                                                                                                                                                                  33.7%;
57.1%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-10-245-871-501
  XU, MINZHEN
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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US-10-200-708-291
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LENGTH: 17
    APPLICANT:
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TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

FILE REPERENCE: REH-2015

CURRENT APPLICATION NUMBER: US/10/253,286

CURRENT FILING DATE: 2003-01-13

PRIOR PAPLICATION NUMBER: 10/197,000

PRIOR FILING DATE: 2002-07-17

PRIOR PLING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 905

SOFTWARRE: Patentin Ver: 2.1

SEQ ID NO 510

LENGTH: 17
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            TITLE OF INVENTION: ALMALANA TITLE OF INVENTION TARENT AND TARENT AND TARENT AND TARENT APPLICATION WOMBER: US/10/253,286
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2002-01-13
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER: OF SEQ ID NOS: 905
SOFTWARE: PATENT NET: 2012
SOFTWARE: PATENT NET: 2013
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                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 510, Application US/10253286
Publication No. US2004005881A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
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GENERAL INPORMATION:
APPLICANT: HUMPHREYS, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: C-term amidated US-10-253-286-510
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Homo sapiens
XU, MINZHEN
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4 IYMNGTM 10
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9 IYMNGTM 15
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APPLICANT:
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TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
FILE REFERENCE: 17999-001
CURRENT APPLICATION NUMBER: US/10/200,708
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/351,036
PRIOR RILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 60/092,346
PRIOR APPLICATION NUMBER: 60/102,346
PRIOR APPLICATION NUMBER: 60/115,145
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PALENTING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 672
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APPLICANT: Chamberlin, Mark A.
APPLICANT: Chamberlin, Mark A.
APPLICANT: Drummond, Bruce J.
APPLICANT: McElver, John A.
TITLE OF INVENTION: RAD51 Polypeptides
FILE REFERRACE: 0556D
CURRENT APPLICATION NUMBER: US/10/246,581
CURRENT APPLICATION NUMBER: US 09/246,963
PRIOR PILING DATE: 1999-02-09-18
PRIOR FILING DATE: 1999-02-09
PRIOR PILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PASSEQ for Windows Version 3.0
SENGTH: 13
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; ORGANISM: Human immunodeficiency virus
US-10-200-708-291
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Publication No. US20030097680A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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42, Appl
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Sequence 124, App
Sequence 25, Appl
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Patent No. 5217869
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Sequence 19, Appl
Sequence 17, Appl
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Sequence 51, A
Sequence 52, A
Sequence 49, A
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14.341 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-45-424-124

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US-08-173-887-3

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US-09-294-987-4

US-09-294-987-4

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US-09-208-163-11

US-09-208-163-11

US-09-665-362A-18

US-09-665-362A-18

US-09-665-362A-18

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US-09-665-362A-18

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US-09-665-362A-13

US-09-665-362A-13

US-09-69-305-51

US-08-476-000-49

US-08-476-000-49

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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US-09-061-7 US-09-142-3 US-08-842-3 US-08-838-5 US-08-04-6 US-08-08-65-5 US-08-014-9 US-08-014-9 US-08-691-6 US-08-691-6 US-08-691-6 US-08-171-6 US-08-171-6 US-08-171-6 US-08-171-6 US-08-171-6 US-08-171-6 US-08-171-6 US-08-171-6 US-09-171-6	IGN CCY US 0, 977	Score 13; DB Pred. No. 3e+ 2; Mismatches
	ALIT. 16, Application US/08193977 16, Application US/08193977 18, Application US/08193977 18, ANT: COLEMAN, KEVIN R. ANT: COLEMAN, KEVIN G. OF INVENTION: P944CDC2 CELL OF INVENTION: P945ILIOMAVIRU TO FECULATION: PAPTILIOMAVIRU TO FECULATION: PAPTILIOMAVIRU TO FECULATION BALTA: UM TYPE: FIOPPY disk TO FECULATION BALTA: UM TYPE: FIOPPY disk FOUNT SYSTEM: PC-DOS/MS-DOS FWARE: DATA: UM TYPE: FIOPPY disk FOUNT SYSTEM: DC-DOS/MS-DOS FWARE: DATA: UM TYPE: FIOPPY disk FOUNT SYSTEM: DS-DOS FWARE: DATA: UM TYPE: FIOPPY disk FOUNT SYSTEM: DS-DOS FWARE: DATA: ULCATION NUMBER: 33,208 SSIFICATION: 530 MSTAGENT INFORMATION: ERRORINS, ROBERTA L. ISTRATION NUMBER: 5999 BERNOK: (415) 327-3231 TION FOR SEQ ID NO: 16: MAUDEDNESS: SINGLE SINGLE TYPE: POPLICE 977-16	% % .:
	ion RES RES RES RES RES RES RES RE	vat
557.1 577.1	1 1 1 1 31-97-16 Luence 116, Application US/08 ent No. 562501 APPLICANT: WEBSTER, KEVIN APPLICANT: WEBSTER, KEVIN APPLICANT: COLEMAN, REWIN TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: PAPLICANT: ADDRESSEE: 34 CORRESPONDENCE ADDRESS: ADDRESSEE: RED & ROBINS STREET: COUNTRY: G.5 BRYANT STREET COUNTRY: UNITED STATES O ZIP: 94301 COMPUTER: FADDABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compation MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compation MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compation MEDIUM TYPE: G.5 BRYANT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/O FILING DATE: 08-EB-1994 CLASSIFATION S30 ATTORNEN' AGENT INFORMATION: NAME: ROBINS, ROBERTA L. REJECTATION: TELEPAX: (415) 327-3231 TELECOMMUNICATION INFORMATI TELECOMMUNICATION INFORMATI TELEPAX: (415) 327-3231 TELEFAX: (415) 327-3231 TELEFAX: (415) 327-3231 TELEFAX: (415) 327-3231 TELEFAX: (415) 327-3231 TOPOLOGY: linear MOLECULE TYPE: peptide	Ë
	T 1 -193-977-16 uence 16, Appient No. 56250 NERAL INFORMATA APPLICANT: CAPPICANT: CAP	Match Local Si
22 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	S-08 S-08 S-08 S-08 GE	Query Match Best Local Matches
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US-08-466-424-124

Sequence 124, Application US/08456424

Sequence 124, Application US/08456424

Sequence 126.

Sequence 127999

GENERAL INFORMATION:

APPLICANT: SATTERTHWAIT JR., ARNOLD C.

APPLICANT: CABEZS, EDELMIRA

APPLICANT: CABEZS, EDELMIRA

TITLE OF INVENTION: SYNTHETIC, STABILIZED, THREE-DIMENSION

TITLE OF INVENTION: POLYPEPTIDES

UNMERS OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: Virginia
COUNTRY: United States
Z19: Z2313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC-DCS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,305
FILING DATE: 08-APR-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: SE 9002684-0
FILING DATE: 17-ANG-1990
ATTORNEY/AGENT INFORMATION:
NAME: CTANG-FRUTY, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 003300-286
TELEDENOME: (703) 856-6620
                                                                                                                                                                                                                            APPLICANT: AHLBORG, Niklas
APPLICANT: BERZINS, Klavs
APPLICANT: BERZINS, Klavs
APPLICANT: BERZINS, Klavs
APPLICANT: BERZINS, Ravs
APPLICANT: BERZINS, Ravs
TILLE OF INVENTION: NEW PEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%; Score 12; DB 1;
100.0%; Pred. No. 3e+05;
tive 0; Mismatches 0
                                                                                                               RESULT 4
US-07-569-305-67
Sequence 67, Application US/07969305
; Patent No. 5609972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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SVI 4
SVI 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: AHLBORG, Niklas
APPLICANT: AHLBORG, Niklas
APPLICANT: BERZINS, Klavs
APPLICANT: BERZINS, Klavs
APPLICANT: BERZINS, Klavs
APPLICANT: BERZINS, Riavs
APPLICANT: Now PEPTIDES AND THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
CONTRY: United States
ACOUNTRY: United States
ACOMPUTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPUTER: IBP PC compatible
COMPUTER: BERZINS PC-DOS/MS-DOS
COMPUTER: COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                Score 13; DB 6; Length 5; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                           ;Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,305
FILING DATE: COA-APR-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%; Score 12; DB 1; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                 61.9%; Scor.
75.0%; Pred. No. sc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 003300-286
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 08-APR-1993
CLASSIFICATION: 530
PRICR APPLICATION DATA:
APPLICATION NUMBER: SE 9002684-0
FILING DATE: 17-A0G-1990
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Peury, Sharon E
                                                                                                                                                    NUMBER OF SEQUENCES: 121
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/255,906
FILING DATE: 11-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 66, Application US/07969305
Patent No. 5609872
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 amino acids
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMIA 5
                                                                                                                                                                                                                                             SEQ ID NO:19:
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US-07-969-305-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-969-305-66
                 RESULT 2
5217869-19
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TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA FILE REFERENCE: P-AS 3337
CURRENT APPLICATION NUMBER: US/09/173,887
CURRENT FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%; Score 12; DB 3; Length 4; 100.0%; Pred. No. 3e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4;
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Pred. No. 3e+05;
                                            CLASSIFICATION:
CLASSIFICATION WUBBER: US 07/822,011
FILING DATE: ABANDONED
CLASSIFICATION: 435
APPLICATION NUBBER: PCT/US/91/02650
FILING DATE: 18-APR-1991
CLASSIFICATION: 435
APPLICATION NUBBER: US 07/615,715
FILING DATE: 20-NOV-1990
CLASSIFICATION WUBBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)
CLASSIFICATION NUBBER: US 07/510,706
FILING DATE: 18-APR-1990 (ABANDONED)
CLASSIFICATION NUBBER: 32,165
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, DAVID L.
REGISTRATION NUBBER: 32,165
REFERENCE/DOCKET NUBBER: UTSD:432/PAR
TELEPHONE: (713) 789-2679
TELEFROMUNICATION INFORMATION:
TELEPHONE: (713) 789-2679
TELEFROMUNICATION INFORMATION:
TELEFROMUNICATION INFORMATION:
TELEFROMUNICATION INFORMATION:
TELEFROMUNICATION INFORMATION:
TELEFROMUNICATION OF 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/08842306B
Patent No. 6271197
GENERAL INFORMATION:
APPLICANT: Berlin, Vivian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-173-887-3
; Sequence 3, Application US/09173887
; Patent No. 6245884
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%; s
100.0%;
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Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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STRANDEDNESS: single
APPLICATION NUMBER:
FILING DATE: 16-FEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: mammalian
                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VIA 4
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APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: REIS, YUYAL
APPLICANT: JAMES, GIX L.
TITLE OF INVENTION: TRANSFERASE INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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Pred. No. 3e+05;
3; Mismatches 0; Indels
                                                                   COMPUTAT: USB

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: Patentin Release #1.0, Version #1.25
CURBUT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,424
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/224,059
FILING DATE: 08-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: BOLICENIC, KAEL
REGISTRATION NUMBER: 28,807
REGISTRATION NUMBER: 28,807
TELEPRAK: 415-434-0792
TELEFRAK: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSES: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: TEXAS COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/08429964 Patent No. 5962243 GENERAL INFORMATION:
      755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%;
25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide US-08-456-424-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                      PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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CLASSIFICATION:
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                                                             USA
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                    CITY: PAI
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
TELEX: 7
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; Sequence 11, Application US/09268163B
; Patent No. 6353091
; CEMERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schoqse, Stephanie
; TILLS OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hook, Vivian Y.H.

TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA FILE REPERBNCE: P-AS 3515
CURRENT APPLICATION NUMBER: US/09/294,987
CURRENT FILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: US 09/173,887
PRIOR FILING DATE: 1998-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MABER: US/08/838,973B
FILING DATE: 23-Apr-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Lens.
5. 3e+05;
0;
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100.0%; Pred. No. 3e+05;
ive 0; Mismatches 0
                                                                                                                                                                                                                                   NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-074.05
TELECOMMUICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 57.1%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 3e+ Matches 3; Conservative 0; Mismatches
                                                                                                                                                                       APPLICATION NUMBER: US 08/631,319
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09294987
Patent No. 6313268
                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Best Local Similarity
Matches 3; Conserv
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US-09-294-987-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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US-09-268-163-11
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SEQ ID NO 4
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Levin, David
Ohya, Yoshikazu
Damagnez, Veronique
Smith, Susan
TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING
ANTI-FUNGAL AGENTS, AND USES RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                              CITY: BOBLOL.
STATE: MA
COUNTRY: USA
ZID: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDER: US/08/42,306B
FILING DATE: 33-Apr.1997
PRIOR APPLICATION NUMBER: US 08/771,212
PRIOR APPLICATION NUMBER: US 08/631,319
FILING DATE: 11-APR.1996
ATTORNEY/AGRNT INFORMATION:
NAME: VINCENT, MATCHEW P.
RECISTRATION NUMBER: 36,709
RECOMMUNICATION INFORMATION:
TELEPRAS: 617-832-1000
TELEFAX: 617-832-1000
TELEFAX: 617-832-7000
JENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.1%; Score 12; DB 3; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0
                                                                                                                                              NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: ONE POST Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOLECULE TYPE: period SEQUENCE DESCRIPTION: SEQ ID NO: 19: US-08-842-306B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08838973B
Patent No. 6277564
GENERAL INFORMATION:
APPLICANT: Berlin, Vivian
Damagnez, Veronique
Smith, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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US-08-838-973B-17
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NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 75.03
Matches 3; Conservative
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                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 3; Conserv
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                   SOFTWARE: 1
SEQ ID NO 2
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100.0%; Pred. No. 3e+05;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: COTTON, Rochard William Arthur APPLICANT: COTTON, Rochard Milliam Arthur APPLICANT: COTTON, Rochard William Arthur TTLE OF INVENTION: PEPTIDE DERIVATIVES FILE REFERENCE: 1991-174
CURRENT APPLICATION NUMBER: US/09/308,175A
CURRENT FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: PCT/GB97/03199
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 8
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US-09-601-178-2
Sequence 2, Application US/09601178
Sequence 2, Application US/09601178
Patent No. 6548306
GENERAL INFORMATION:
APPLICANT: ADMON, Arie
APPLICANT: PALITELI, Yoav
APPLICANT: BAUNELI, Silvia
APPLICANT: SLOTKY, Ronit
TITLE OF INVENTION: PLACENTAL PROTEIN 13
FILE REFERENCE: ADMON=1
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: PCT/1L99/00036
PRIOR PILING DATE: 1999-01-13
PRIOR PILING DATE: 1999-01-21
PRIOR FILING DATE: 1999-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
CURRENT APPLICATION NUMBER: US/09/268,163B
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 60/077,901
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-308-175A-8
; Sequence 8, Application US/09308175A
: Patent No. 6355617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.1%;
Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                                                                                                                                                             Query Match
Best Local Similarity 100..
                                                                                                                                                    TYPE: PRT ORGANISM: Conus geographus
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1 VAK 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BROWN, MICHAEL S.
APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: GOLDSTEIN, JOSEPH L.
TITLE OF INVENTION: METHODS OF ASSAYING FARNESYL TRANSFERASE
TITLE OF INVENTION: WELSO, 10750: 2494020.
CURRENT APPLICATION NUMBER: US/09/665,362A
CURRENT FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: 07/937,893
PRIOR PILING DATE: 1992-12-22
PRIOR APPLICATION NUMBER: 07/615,715
PRIOR PELING DATE: 1990-11-20
PRIOR FILING DATE: 1990-11-20
PRIOR FILING DATE: 1990-11-20
PRIOR SPELICATION NUMBER: 07/510,706
PRIOR FILING DATE: 1990-11-20
PRIOR SEQ ID NOS: 52
COFTWARE: PATCHIN VOE: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hook, Vivian Y.H.
TITLE OF INVENTION: SECRETASES RELATED TO ALZHEIMER'S DEMENTIA FILE REFERENCE: P.AS. 4579
CURRENT APPLICATION NUMBER: US/09/797,543
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION WHERE: US 09/173,887
PRIOR FILING DATE: 1998-10-16
                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%; Score 12; DB 4; Length 4;
100.0%; Pred. No. 3e+05;
ive 0; Mismatches 0; Indels
Score 12; DB 4;
Pred. No. 3e+05;
0; Mismatches
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                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09797543
Patent No. 6627409
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
  57.1%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
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US-09-665-362A-18

0; Gaps Query Match 57.1%; Score 12; DB 4; Length 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels

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Search completed: August 12, 2004, 06:55:49 Job time: 19 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 12, 2004, 06:12:47; Search time 1.56762 Seconds (without alignments) 1043.144 Million cell updates/sec

US-09-890-463-2 83 1 SVIAKQMTYKVYMSGTV 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		protein of short-c	hypothetical prote	delta-(L-alpha-ami	surfactin syntheta	surfactin syntheta	hypothetical prote		sugar transport sy	hypothetical prote	hypothetical prote		odorant receptor (regulatory protein	Ä	ein	균	phosphoserine tran	phosphoserine amin	hypothetical prote	probable membrane	hypothetical prote	alpha-aminoadipyl-	hypothetical prote	probable lipoprote	probable lipoprote	probable polymeras	lipoprotein yajg p	probable polymeras	4 6 1000 4 6 1000 1000
<u> </u>		G96956	T43498	A40889	I40486	I40485	E86687	C97225	F83890	G83962	T10634	AH2136	A40745	S64488	A70233	G70394	H71473	F81816	H81059	T29945	AG0182	S59262	YGCEVC	A69445	AI0383	AH0557	D85540	B64773	H90689	ロンドロフュ
E	;	7	7	7	7	N	N	7	7	7	7	7	7	7	7	~	7	7	7	~	7	7	Н	~	7	~	7	0	7	c
Length		398	424	3770	3587	3588	218	263	285	294	870	1086	191	170	277	337	346	368	368	459	786	846	Н	140	Q)	192	226	N	226	227
Query		4.	51.8	51.8	49.4	49.4	48.2	48.2	48.2	48.2	48.2	48.2	47.0	47.0	47.0	47.0	47.0	47.0	47.0	47.0	47.0	47.0	47.0	45.8			45.8	45.8	45.8	4 7 8
9,000	1 0 0	45	43	43	41	41	40	40	40	40	40	40	39	39	39	39	39	39	39	39	39	39	39	38	38	38	38	38	38	3,8
Result		1	7	3	4	5	9	7	œ	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	50

probable membrane- protochlorophyllid	thymidine kinase (exo-alpha-1,4-gluc	probable serine/th topoisomerase IV ${ m c}$	pertussis toxin ch	Leucine dehydrogen	leucine dehydrogen	probable serine/th	UDP-N-acetylmuramo	UMP synthase - sli	hypothetical prote	protochlorophyllid	coiled coil protei	peptide synthetase
F95952 B36716	KIBEMV H70011	S38035 S73358	F25973	E86605	F72020	G81436	F84955	S03826	B86899	S10176	T41515	I40457
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234	353 554	560 635	227	351	351	384	440	478	552	563	1184	2560
45.8	45.8 45.8	45.8	44.6	44.6	44.6	44.6	44.6	44.6	44.6	44.6	44.6	44.6
38	38 38	80 80 80 80	37	37	37	37	37	37	37	37	37	37
30 31	32 33	3.4	36	37	38	39	40	41	42	43	44	45

G96956	
protein of short-chain alcohol dehydra (C.Species: Clostridium acetobutylicum	protein of short-chain alcohol dehydrogenase family [imported] - Clostridium acetobutylid C.Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_r	C.Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
R;Nolling, J.; Breton, G.; Omel	chenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.
.; Daly, M.J.; Bennett, G.N.; K J. Bacteriol. 183, 4823-4838. 2	.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Co	A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A;kererence number: Aybyou; MoiD:zissyszs; FMiD:zissyszs A:Accession: G96956	U:Z1339325; FMID:Z1339323
A; Status: preliminary	
A; Residues: 1-398 < KUR>	
A/Cross-ferences: GB:ABUOL43/; FIDN:AAA/8442.1; FID:915 A/Experimental source: Clostridium acetobutylicum ATCC824	A;Cross-Terefrences: GB:AEUU143/; FIDN:AAN/0842.1; FID:GISU23320; GSFDB:GNU0100 S. Maxperimental source: Clostridium acetobutylicum ATCC824
C;Genetics: A;Gene: CAC0462	
C, Superfamily: Xylella fastidiosa hypothetical protein XF1835	sa hypothetical protein XF1835
Query Match	
Best Local Similarity 47.1%; Matches 8; Conservative	; Fred. No. 3.2; 2; Mismatches 7; Indels 0; Gaps 0;
QY 1 SVIAKQMIYKVYMSGTV 17	17
Db 224 SYIGSPRTYKIYREGTI 240	240

hypothetical protein DKFZp586C1021.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T43499
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, December 1999
A;Reference number: Z22515
A;Accession: T43498
A;Status: prellimary
A;Molecule type: mRNA
A;Residues: 1-424 cAAA>
A;Gesidues: 1-424 cAAA>
A;Cross-references: EMBL;AL133640
A;Experimental source: adult uterus; clone DKFZp586C1021
C;Genetics:
A;Note: DKFZp586C1021.1

Gaps ·. Query Match 51.8%; Score 43; DB 2; Length 424; Best Local Similarity 43.8%; Pred. No. 7.8; Matches 7; Conservative 5; Mismatches 4; Indels

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2

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iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucell, Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetella, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Schiguchi, J.; Sckowska, A.; Serox akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, J.; Sckowska, A.; Serox A; Julhers, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, J.; Sckowska, A.; Serox A; Juthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama, A; Juthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama, A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Accession: C69718
A; Residues: I-3587 ckUN>
A; Residues: I-3587 ckUN>
A; Residues: I-3587 ckUN>
A; Rossinental source: Strain 168
A; Experimental source: Strain 168
B; Fabret, C.; Quentin, Y.; Guiseppi, A.; Busuttil, J.; Haiech, J.; Denizot, F.
B; Dance, M.; Barat, March 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Modecule type: DNA
A; Modecule type: DNA
A; Modecule type: DNA
A; Modecule type: DNA
A; Modecule type: DNA
A; Modecule type: DNA
A; Residues: 1-32, F', 34-41, 'G', 43-109, 'D', 111-114, 'G', 116-138, 'V', 140-258, 'W', 260-308, 'A
1756-1914, 'PK', 1917-2138, 'SRL', 2142, 'DSLN', 2146-2444, 'Q', 2446-2712, 'H', 2714-2722, 'H', 272
A; Cross-references: EMBL: X72672; NID:9516358; PIDN: CAA51223.1; PID:9516360
R; Funa, S., Fujishima, Y.; Corbell, N.; D'Souza, C.; Nakano, M.M.; Zuber, P.; Yamane, K.
Nucleic Acids Res. 21, 93-97, 1993
A; Title: Nucleotide sequence of 5' portion of srfa that contains the region required for A; Reference number: S35517; MUID:93181186; PMID:8441623
A; Accession: S35517; MUID:93181186; PMID:9216347
A; Status: significant sequence differences
A; Modecule type: DNA
A; Cross-references: EMBL:D13262; NID:9216345; PID:9216347
A; Experimental source: strain 168 trpC2
R; Borchert, S; Patli, S.S; Marahiel, M.A.
FEMS Microbiol Lett. 92, 175-180, 1992
A; Title: Identification of putative multifunctional peptide synthetase genes using highly A; Reference number: S25658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 168, C., 170-171, 281-283;514-595, 597-647, R., 649-679, ELL., 683-693, DKR., 697, A;Cross-references: BMBL:X65835, NID:940202; PIDN:CAA46678.1; PID:940203
A;Experimental source: strain ATCC 21332
C;Comment: This protein contains several amino acid-activating domains for the synthesis the amino-terminal region of this protein, appear to be required for the development of C;Genetics:
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C,Superfamily: surfactin synthetase, acetate-CoA ligase homology, acyl carrier protein homology surfactin synthetase; acetate-CoA ligase homology, saction; ligase, phosphopantetle; C,Superfamily: solutionic blosynthesis, carrier protein; duplication; ligase, phosphopantetle; 5:11-951/Domain: acetate-CoA ligase homology <ACL1>
F;068-1035/Domain: acetate-CoA ligase homology <ACL2>
F;1036-1481/Domain: acetate-CoA ligase homology <ACL2>
F;2013-2081/Domain: acetate-CoA ligase homology <ACL2>
F;2013-2081/Domain: acetate-CoA ligase homology <ACL2>
F;2013-2081/Domain: repeat <RFT2>
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surfactin synthetase component I - Bacillus subtilis
N;Alternate names: competence protein srfAA; surfactin production protein srfAA; surfact
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F;3041-3108/Domain: acyl carrier protein homology <ACP3>
F;999,2045,3073/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
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Best Local Similarity
Matches 7; Conserv
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delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase - Emericella nidulans
C; Belta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase - Emericella nidulans
C; Beta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase - Emericella nidulans
C; Bate: 27-Mar.1992 #sequence_revision 27-Mar.1992 #text_change 03-Nov-2000
C; Accession: A40889; Sidéde
B; MacCabe, A.P.; van Liempt, H.; Palissa, H.; Unkles, S.E.; Riach, M.B.R.; Pfeifer, E.;
J. Biol. Cham. 266, 12646-12654, 1991
A; MacCabe, A.P.; van Liempt, H.; Palissa, H.; Unkles, S.E.; Riach, M.B.R.; Pfeifer, E.;
A; Title: delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase from Aspergillus ni A; Reference number: A40889
A; Molecule type: DNA
A; Residues: 1-3770 cMAC>
A; Cross-references: GB:X54853; NID:g2318; PIDN:CAA38631.1; PID:g2319
A; Molecule type: DNA
A; Residues: 1-3770 cMAC>
A; Cross-references: GB:X54853; NID:g2318; PIDN:CAA38631.1; PID:g2319
A; Molecule type: DNA
A; Residues: 1-3770 cMAC>
A; Cross-references: GB:X54853; NID:g2318; PIDN:CAA38631.1; PID:g2319
A; Molecule type: DNA
A; Gene: ac;
A; Gene: 
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Surfactin synthetase component II - Bacillus subtilis

Nyllcriate names: surfactin synthetase sifA2; surfactin synthetase/competence protein surfactin synthetase sifA2; surfactin synthetase conforms: acid-amino-acid ligase (EC 6.3.2.)

C.Species: Bacillus subtilis

C.Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text change 03-Nov-2000

C.Accession: 140486; S60866; C69718; S46968; S35518; S25688; S34986

R;Cosmina, P.; Roddiguez, F.; de Perra, F.; Grandi, G.; Perego, M.; Venema, G.; van Sind

A.Title: Sequence and analysis of the genetic locus responsible for surfactin synthesis

A,Reference number: 140486; MUID:93360813; PMID:835509

A,Residues: translated from GB/EMBL/DDBJ

A,Molecule type: DNA

A,Residues: 13587 cRES

A,Cross-references: EMBL:X70356; NID:9396480; PIDN:CAA49817.1; PID:9396482

A,Residues: 13587 cRES

A,Residues: 13587 cRES

A,Residues: 15-55-63.1995 acrea in William William in the coding region of the fourth a A,Reference number: S60866; WUID:95272393; PMID:7752896

A,Molecule type: DNA

A,Reference number: S60866; WUID:95272393; PMID:7752896

A,Molecule type: DNA

A,Reference number: S60866; WUID:95272393; PMID:7752896

A,Molecule type: DNA

A,Reference number: S60866; WUID:95272393; PMID:7752896

A,Recession: S6086

A,Rocession: S6086

A,Rocession: S6086

A,Rocession: S6086

A,Rocession: S0086

A,Rocession: S0086

A,Rocession: S0086

A,Rocession: S0086

A,Ruthors: F.; Ogaswarra, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Rebrer, C.; Perrari, E.

A, Ehrlich, S. D: Encullet, S. D: Eruschi, C.; Fullita, M.; Fullita, Y.; Fuma, S.; Galizzi, A.; Galler

A,Ruthors: Foulger, D.; Fritz, C.; Fullita, M.; Fullita, Y.; Fuma, S.; Galizzi, A.; Galler
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50.0%; Pred. No. 71;
ive 3; Mismatches 5; Indels
                     16
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                     SVIAKOMTYKVYMSGT
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Matches 8; Conserv
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hypothetical protein CAC2643 [imported] - Clostridium acetobutylicum CSP225.

hypothetical protein CAC2643 [imported] - Clostridium acetobutylicum CSP02125.

c)Species: Calostridium acetobutylicum
C;Species: Calostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: C97225
R;Nobling, J.; Bennett, G.N.; Kconin, E.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Kconin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97225
A;Actus: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis subsp. lactis C; Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C; Accession. B8668r, Winoker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001 A; Fittle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A; Reference number: A86625; WUID:21235186; PMID:11337471
C;Keywords: antibiotic biosynthesis; carrier protein; phosphopantetheine; phosphoprotein 5.507-956/Domain: acetate-CoA ligase homology <ACL1> F;974-1042/Domain: acetate-coA protein homology <ACP1> F;974-1042/Domain: acetate-coA protein homology <ACP1> F;1043-1488/Domain: repeat <RP71>
                                                                                                                                               F;1549-1993/Domain: acetate-CoA ligase homology <ACL2>
F;2011-2079/Domain: acyl carrier protein homology <ACP2>
F;2080-2527/Domain: repeat <RPT2>
F;2689-3025/Domain: acetate-CoA ligase homology <ACL3>
F;3042-3109/Domain: acyl carrier protein homology <ACL3>
F;3042-3109/Domain: acyl carrier protein homology <ACP3>
F;006,2043,3074/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
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A;Residues: 1-218 <2TO>
A;Cross-references: GB:AE005176; PID:g12723383; PIDN:AAK04599.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yfaA
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ATCC824
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43.8%; Pred. No. 1.68+02;
Twismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 2
Pred. No. 14;
2; Mismatches
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Pred. No. 17;
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Best Local Similarity 43.000
T; Conservative
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Best Local Similarity
7; Conserv?
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             Authoric Nucleotide sequence of 5' portion of srfA that contains the region required for A; Reference number: 835517; MUID: 93181186; PMID: 8441623
A; Reference number: 835517; MUID: 93181186; PMID: 8441623
A; Accession: 835517
A; Cross-references: EMBL: D13265; NID: 9318136345; PID: 9316346
A; Robert type: DNA
A; Cross-references: EMBL: D13262; NID: 9316345; PID: 9316346
A; Robert sequence of complete, the nucleotide sequence was submitted to the EMBL Robano, M.M.; Magnuson, R.; Myers, A.; Curry, J.; Grossman, A.D.; Zuber, P.
J. Bacteriol: 173, 1770-1778, 1991
A; Title: srfA is an operon required for surfactin production, competence development, an A; Reference number: A37323; MUID: 91154134; PMID: 1847909
A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Residues: 1-46, EW, 49-145, II, 147-150, II', 152, 'AN', 155-280, II', 282-307, 'SF', 310-384 A; Asharon, M. M.; Yis II', And Sharon, M. M. Yis II's Appleance of Sharon, M. M. Yis II's App
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A;Note: srfAA is the first gene of the srfA operon
C;Superfamily: surfactin synthetase; acetate-CoA ligase homology; acyl carrier protein h
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A,Residues: 3249-3271,'A',3273-3316,'R',3318-3451,'Y',3453-3483,'DE',3486-3487,'DAGL',34
A,Cross-references: EMBL:X72672; NID:g516358; PIDN:CAA51222.1; PID:g516359
A,Experimental source: strain 168 trpC2
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C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Nov-2000
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Nov-2000
C;Accession: I40485; B69718; S35517; A37323; S4667; A43705; S34985
R;Cosmina, P.; Rodriguez, F.; de Ferra, F.; Grandi, G.; Perego, M.; Venema, G.; van Sind Mol. Microbiol. 8, 821-831, 1993
A;Title: Sequence and analysis of the genetic locus responsible for surfactin synthesis A;Reference number: I40485; MUID:93360813; PMID:8355609
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R;Fuma, S.; Fujishima, Y.; Corbell, N.; D'Souza, C.; Nakano, M.M.; Zuber, P.; Yamane, K.
Nucleic Acids Res. 21, 93-97, 1993
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A;Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12142.1; PID:g2632634
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A;Reference number: S46967
A;Accession: S46967
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A, Status: translated from GB/EMBL/DDBJ
A, Molecule type: DNA
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803 SKLAKRHNYSVYFSG 817
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VTPECLTYLIYTSGS 624
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         A;Residues: 1-870 <BEV>
                                                                                                                                                                                   A; Gene: ATSP:T13K14.80
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C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: O1-Dec-2000 #text_change 15-Jun-2001
C;Accession: G83962
R;Takami, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83962
A;Accession: G83962
A;Residues: preliminary
A;Moolecule type: DNA
A;Residues: 1-294 <STO>
A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06222.1; GSPDB:GNOC
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2503
C;Superfamily: conserved hypothetical protein H11714
                                                                                                                                                                                                                                              Giger transport system (permease) BH1926 (imported] - Bacillus halodurans (strain C-125) Sugar transport system (permease) BH1926 (imported] - Bacillus halodurans (c;Species: Bacillus halodurans (c;Species: Bacillus halodurans (c;Species: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: R83890

R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000

A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A.Reference number: A83650; MUID:20512582; PMID:11058132

A.Accession: R83890

A.Status: Preliminary
A.Molecule type: DNA
A.Residues: 1-285 <2TO
A.Residues: BNA
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Pred. No. 18;
2; Mismatches 3; Indels
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Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
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244 ARQMDYGMIMSGT 256
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133 EQLGYKVYLTSTI 145
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Matches 6; Conserv
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
NDA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Superfamily: peptide synthetase ppsE; acetate-CoA ligase homology; acyl carrier protei C.Keywords: carrier protein; phosphopantetheine; phosphoprotein F;1015/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
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C;Date: 21-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C;Accession: A40745 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C;Accession: A40745 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
R;Reseler, K.J.; Sullivan, S.L.; Buck, L.B.
Cell 73, 597-609, 1993
A;Title: A zonal organization of odorant receptor gene expression in the olfactory epiths
A;Reference number: A40745; MUID:93258822; PMID:7683976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2136
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A;Cross-references: GB:BA000019; PIDN:BAB74346.1; PID:g17131740; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Cross-references: GB:L14568; NID:g293757; PIDN:AAA39852.1; PID:g293758
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A;Introns: 72/3; 105/3; 257/2; 328/2; 635/1; 685/3; 724/3
C;Superfamily: Arabidopsis thaliana hypothetical protein T13K14.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microcystin synthetase B [imported] - Nostoc sp. (strain PCC 7120)
A;Cross-references: EMBL:AL080282; GSPDB:GN00062; ATSP:T13K14.80
A;Experimental source: cultivar Columbia; BAC clone T13K14
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.2%; Score 40; DB 2; Length 1086; 46.7%; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                          48.2%; Score 40; DB 2; Length 870; ilarity 53.3%; Pred. No. 56; Conservative 2; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
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Search completed: August 12, 2004, 06:13:50 Job time : 3.56762 secs
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| SIFFKEMAYKMHVFDTV 86
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26 AKELGYKIYLVG 37
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 28-Jul-2000
C;Accession: A70233
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Sow, D.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Wenter, J.C.
A;Reference number: A70233
A;Accession: A70233
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A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Crivellone, M.D.
J. Biol. Chem. 269, 21284-21292, 1994
A;Title: Characterization of CBP4, a new gene essential for the expression of ubiquinol-
A;Reference number: A53928; MUID:94342301; PMID:8063753
A;Accession: A53928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residudes: 1-170 <=mBb.:272959; NID:g1323307; PID:e243557; PID:g1323308; MIPS:YGR174c
A;Experimental source: strain S288C
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                                                                                                                                                                                                                                                                 regulatory protein CBP4 precursor - yeast (Saccharomyces cerevisiae)
NiAlternate names: protein G712; protein YGR174c
C.Species: Saccharomyces cerevisiae
C.Species: 3accharomyces cerevisiae
C.Spacie: 17-May_1996 #sequence_revision 17-May-1996 #text_change 21-Jul-2000
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A;Residues: 1-64,'F',66-170 <CRI>
A;Cross-references: GB:U10700; NID:g505645; PIDN:AAA61566.1; PID:g505646
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C;Superfamily: Borrelia burgdorferi hypothetical protein BBG17
   Indels
   3.
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                                                                                                                                                                                                                                                                                                                                                                                C,Accession: S64488, A33928
R;Hebling, U.; Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64003
A;Accession: S64488
   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: SGD:S0003406; MIPS:YGR174c A;Map position: 7R A;Genome: nuclear
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Best Local Similarity 61...
Lac 8; Conservative
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   8; Conservative
                                                                                                                  5 ICKPLTYKVIMS 16
                                                          3 IAKQMTYKVYMS 14
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   Matches
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PlsX protein - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: Ob-May-1998 #sequence_revision 08-May-1998 #text_change 28-Jul-2003
C;Accession: G70394
R;Deckert, G; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE000723; NID:g2983569; PIDN:AAC07145.1; PID:g2983573; GB:AE000657.
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                             Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: G70394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: phospholipid biosynthesis protein,
1 SVIAKOMIYKVYMSGTV 17
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                   Copyright
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OM protein - protein search, using sw model

August 12, 2004, 06:12:47; Search time 1.04508 Seconds (without alignments) 847.008 Million cell updates/sec Run on:

US-09-890-463-2 83 Perfect score:

1 SVIAKQMTYKVYMSGTV 17 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P27742 emericella	bacil	bacillus	Q9k9z1 bacillus ha		P34985 mus musculu				P57007 neisseria m		P25464 cephalospor									P37824 chlamydomon								vibrio	Q97bv0 thermoplasm		rhodc	P70612 rattus norv
SUMMARIES	ID	ACVS EMENI	SRF2 BACSU	SRF1 BACSU	ENGC_BACHD	SM2A SCHGR	OL7A_MOUSE	CBP4 YEAST	PLSX_AQUAE	SERC NEIMA	SERC NEIMB	SP98 YEAST	ACVS_CEPAC		YAJG ECOLI	BCHL_RHOCA			PTK1_YEAST	PARE MYCPN	MURD BUCAI	CHLB_CHLPT	PYR5_DICDI	CHLB_CHLMO	PPS2_BACSU	YA7B HAEIN	H2B4_VOLCA	H2B3_VOLCA	FABA_VIBPA	FABA_VIBVU	KCY THEVO			IL8A_RAT
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P12045 bacillus su Q9kr69 vibrio choll P43948 haemophilus Q8eu02 oceanobacil Q9zzw7 saccharomyc P41606 pinus thunb Q8r0w0 mus musculu P01451 naja haje a P01451 naja haje a Q97bw9 thermoplasm O33877 pseudomonas	
PURK BACSU YH74_VIBCH MPL FABIN SYE_OCEIH MBI3 YEAST RPOD_PINTH EPPL_MOUSE CX3 NAJHA CX4_NAJHA SUII_THEVO FABA PSEAE	
379 384 483 483 517 1224 60 60 100	
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: Biosynthesis of penicillin and cephalosporin; first step. -!- PTM: The N-terminus is blocked. -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intermediates.
-!- CATALYTIC ACTIVITY: L-2-aminohexanedioate + L-cysteine + L-valine + 3 ATP = N-[L-5-amino-5-carboxypentanoy1]-L-cysteinyl-D-valine + 3 AMP + 3 diphosphate.
-!- COFACTOR: Contains 3 covalently bound phosphopantetheines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=G191;
MEDLINE=91266299, PubMed-2061313;
MEDLINE=91266299, PubMed-2061313;
MEDLINE=91266299, PubMed-2061313;
MEDLINE=91266299, PubMed-2061313;
Maccabe A.P., van Liempt H., Pallissa H., Unkles S.E., Riach M.B.R., Pfeifer E., von Doehren H., Kinghorn J.R.;
"Della-(L-alpha-aminoadipyl)-L-cysteliny-D-valine synthetase from "Della-(L-alpha-aminoadipyl)-L-cysteliny-characterization of the acvA gene encoding the first enzyme of the penicillin biosynthetic pathway.";
J. Biol., Chem. 266:12646-12654(1991).
-!- FUNCTION: Each of the constituent amino acids of the tripeptide acv are activated as aminoacy1-adenylates with peptide bonds increased across through the participation of amino acid thiolester
                                                                                                                                          01-A00-1992 (Rel. 23, Created)
01-A00-1992 (Rel. 23, Last sequence update)
01-B01 (Rel. 41, Last annotation update)
N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase
(EC 6.3.2.26) (Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine
                                                                                                                                                                                                                                                                                                                                                                                                                               Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
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                                                                                                                                                                                                                                                                                                                                                      synthetase) (ACV synthetase) (ACVS)
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InterPro; IPR006163; Pp bind.
InterPro; IPR006162; Ppantne_S
InterPro; IPR000379; Ser_estrs.
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                                                                             STANDARD;
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Euma S., Fujishima Y., Corbell N., D'Souza C., Nakano M.M.,
Zuber P., Yamane K.;
"Nucleotide sequence of 5' portion of srfA that contains the region
required for competence establishment in Bacillus subtilis.";
Nucleic Acids Res. 21:93-97(1993).
                                                                                                                                                                                                     DOMAIN 1 (ADIPATE-ACTIVATING).
DOMAIN 2 (CYSTEINE-ACTIVATING).
DOMAIN 3 (VALINE-ACTIVATING).
ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 2.
PHOSPHOPANTETHEINE (BY SIMILARITY).
PHOSPHOPANTETHEINE (BY SIMILARITY).
PHOSPHOPANTETHEINE (BY SIMILARITY).
THIOESTERASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamane K., Kumano M., Kurita K.;
"The 25 degrees-36 degrees region of the Bacillus subtilis
chromosome: determination of the sequence of a 146 kb segment and
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MEDILNE=933560813; PubMed=8355609;
Cosmina P., Rodriguez F., de Ferra F., Grandi G., Perego M.,
Venema G., van Sinderen D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                51.8%; Score 43; DB 1; Length 3770; 50.0%; Pred. No. 28;
             Pfam; PF00501; AMP-binding; 3.
Pfam; PF00568; Condensation; 3.
Pfam; PF00569; Condensation; 3.
Pfam; PF00505; Thioesterase; 1.
PRINTS; PR00154; AMPBINING.
PROSITE; PS00455; AMP BINDING; 3.
PROSITE; PS0075; ACP DOWAIN; 3.
Ligase; Antibiotic Dowaln; 3.
Ligase; Antibiotic biosynthesis; Multifunctional enzyme; Repeat; Phosphopantetheine.
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15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRFAB OR SRFA2 OR COML OR BSU03490.
Bacillus subtilis.
InterPro; IPR001031; Thioesterase.
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Microbiology 142:3047-3056(1996)
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Best Local Similarity
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ID O1-FEB
DT 10-OCT
DE SUFFAB
OC BACTEIL
OC BA
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MINDLINES-980440103, bubbed-1849177, MINDLINES-980440103, bubbed-1849477, MINDLINES-980440103, bubbed-1849477, Bandan R. Alloni G., Band R. Alloni R. Alloni G., Band R. Alloni G., Band R. Alloni G., Band R. Alloni G., Gayl B. J., Haga K., Duttarhoft A., Malch J., Harwood C. R., Henaut A., Galleston R. Alloni espid G., Gayl B. J., Haga K., Laladeh J., Harwood C. R., Henaut A., Galleston R. Alloni espid G., Gayl B. J., Haga K., Laladeh J., Harwood C. R., Henaut A., Galleston R. Alloni espid G., Gayl B. J., Haga K., Laladeh J., Harwood C. R., Henaut A., Galleston R. Alloni espid G., Gayl B. J., Haga M. J., Hale R. Alloni R. All
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GAIAGRVDLYEPDAFAKRPTIG -> APSPGGLICMSRCIC
ETPDNR (IN REF. 1).
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PERMITS, PRO0550; pp-binding; 3.
PRINTS; PR00154; AMPBINDING.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 3.
PROSITE; PS00455; AMP BINDING; 3.
PROSITE; PS00455; AMP DINDING; 3.
Ligase; Antibiotic biosynthesis; Phosphopantetheine; Sporulation; Multifunctional enzyme; Repeat; Complete proteon
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MSAAVLGV -> KCPPRCSAS (IN REF.

KL -> NV (IN REF. 1).
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R -> C (IN REF. 1).
A -> V (IN REF. 1).
ARLTP -> LRDSLN (IN REF. 1).
E -> Q (IN REF. 1).
ATDLF -> RQICS (IN REF. 1).
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RF -> L (IN REF. 1).
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DOMAIN 3 (D-LEU-ACTIVATING)
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Q -> D (IN REF. 1).
Q -> D (IN REF. 1).
RQA -> AQG (IN REF. 1).
A -> V (IN REF. 1).
L -> W (IN REF. 1).
R -> A (IN REF. 1).
TPA -> SRP (IN REF. 1).
TPA -> SRP (IN REF. 1).
MISSING (IN REF. 1).
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RHV -> ETL (IN REF. 1).
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. Gaps 0; DB 1; Length 3587; 5; Indels Score 41; DB Pred. No. 62; 4; Mismatches 49.4%; 43.8%; 16 1 SVIAKOMTYKVYMSGT Conservative Query Match Best Local Similarity 7; Matches

STANDARD; SRF1_BACSU ID SRF1_BACSU AC P27206; RESULT 3

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PRT; 3588 AA.

RA MEDLINE-98044033; Pubmed-9314377;

RA MEDLINE-98044033; Pubmed-9314377;

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Bruschi C.V., Caddwell B., Capuano V., Carter N.M., Capuano V., Catter N.M., Chois S., Bruschi C.V., Caddwell B., Capuano V., Carter N.M., Chois S., Bruischi C.V., Codnerton I.F., Cummings N.J., Daniel R.A., Ertington J.J., Connerton I.F., Cummings N.J., Daniel R.A., Ertington J., Fabret C., Ferrari E., Foulger D., Emmerson P.T., RA Denizot F., Davine R.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., RA Fitz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghiseppi G., Guy B.J., Haga K., Haiceh Y., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Guiseppi G., Guy B.J., Haga K., Haiceh J., Harwood C.R., Henaut A., Jonis B., Kramanta D., Kasanhara Y., Klaerre-Blanchard M., Klein C., Robayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M., Koetter P., Koningstein G., Kroph S., Kumano M., Koetter P., Mizuno M., Moestl D., Nakai S., Noback M., Roone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Persoctt A.M., Noone D., O'Reilly M., Portetelle D., Porwollik S., Rey M., Reynolds S., Sauto T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Schleich S., Schroeter R., Scoffone F., Schleich S., Schroeter R., Scoffone F., Schleich S., Serror P., Shin B.S., Soldo B., Sorokin A., Tamakoshi A., Tarakashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Tarepstra P., Vanmotte R., Vandenbol M., Vannier F., Vassarotti A., Vanters P., Wipat A., Yanmaco P., Yoshikawa H., Danchin A., Tanaka H., Tanaka H., Takemaru K., Yoshikawa H., Danchin A., Tanaka H., Soshikawa H., Danchin A., Tanaka H., Vannier P., Vassarotti A., Wannotte R., Wannotte R., Wadler E., Voshikawa H., Danchin A., Tanaka H., Vannier P., Vassarotti A., Yannamoto H., Yannae K., Yoshikawa H., Danchin A., Tanaka H., Wannotte R., Watter Squeer M., Sauterin B., Yannae S., Wannae S., Wannae S., "Sequence and analysis of the genetic locus responsible for surfactin synthesis in Bacillus subtilis.";
MOI. Microbiol. 8:821-831(1993). Zuber P, Yamane K.;
"Nucleotide sequence of 5' portion of srfA that contains the region
"required for competence establishment in Bacillus subtilis:";
Nucleic Acids Res. 21:93-97(1993). Yamane K., Kumano M., Kurita K.; "The 25 degrees-36 degrees region of the Bacillus subtilis chromosome: determination of the sequence of a 146 kb segment and Cosmina P., Rodriguez F., de Ferra F., Grandi G., Perego M., Venema G., van Sinderen D.; MEDLINE-93181186; PubMed-8441623; Fuma S., Fujishima Y., Corbell N., D'Souza C., Nakano M.M., SRFAA OR SRFAI OR SRFA OR BSU03480. Bacillus subtilis. Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. 01-AUG-1992 (Rel. 23, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 20-CCT-2003 (Rel. 42, Last annotation update) Surfactin synthetase subunit 1 SEQUENCE FROM N.A. STRAIN=168 / JH642; MEDLINE=93360813; PubMed=8355609; STRAIN=168; MEDLINE=97124189; PubMed=8969502; MEDLINE=98044033; PubMed=9384377; SEQUENCE OF 1-460 FROM N.A. MEDLINE=91154134; PubMed=1847909; identification of 113 genes."; Microbiology 142:3047-3056(1996). Nature 390:249-256(1997). SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI_TaxID=1423; STRAIN=168; STRAIN=168

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fujishima Y., Yamane K.;
A.10 kb nuclectide sequence at the 5' flanking region (32 degrees)
of srfAA of the Bacillus subtilis chromosome.";
Microbiology 141:277-279(1995).
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91358326; PubMed=1715856;
Nakano M.M., Xia L., Zuber P.;
"Transcription initiation region of the srfA operon, which is controlled by the comP-comA signal transduction system in Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO ACTIVATE AND POLYMERIZE THE AMINO ACIDS LEU, GLU, ASP AND VAL. ACTIVATION SITES FOR THESE AA CONSIST OF INDIVIDUAL DOMAINS. COFACTOR: Contains 3 covalently bound phosphopantetheines. PATHWAY: Cyclic peptide antibiotic surfactin biosynthesis. SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                "srfA is an operon required for surfactin production, competence development, and efficient sporulation in Bacillus subtilis."; J. Bacteriol. 173:1770-1778 (1991).
Nakano M.M., Magnuson R., Myers A.M., Curry J., Grossman A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Multifunctional enzyme; Repeat; Complete proteome. | REPEAT | 2 1047 | DOMAIN 1 (GLU-ACTIVATING). | 2 1047 | DOMAIN 2 (LEU-ACTIVATING). | DOMAIN 2 (LEU-ACTIVATING). | DOMAIN 3 (D-LEU-ACTIVATING). | DOMAIN 3 (D-LEU-ACTIVATING). | DOMAIN 3 (D-LEU-ACTIVATING). | DOMAIN 3 (D-LEU-ACTIVATING). | ACYL CARRIER (ACP) 1. | DOMAIN 3 (D44 3110 | ACYL CARRIER (ACP) 2. | DOMAIN 3 (D44 3110 | ACYL CARRIER (ACP) 2. | DOMAIN 3 (D44 3110 | PHOSPHOPANTETHEINE (POTENTIAL). | BINDING 2043 2043 | PHOSPHOPANTETHEINE (POTENTIAL). | BINDING 3074 3074 | PHOSPHOPANTETHEINE (POTENTIAL). | DOMENTIAL). | DOMENTIAL | DOMENTIAL). | DOMENTIAL 
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V -> L (IN REF. 1 AND
G -> A (IN REF. 1).
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                                                                                                                                                                                                                  MEDLINE=95219080; PubMed=7704255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 173:5487-5493(1991)
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-38 FROM N.A.
                                                                                                                                                            SEQUENCE OF 1-64 FROM N.A.
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                                                                                                                                                                                        STRAIN=168;
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Q -> T (IN REF. 1 AND 5).
D -> T (IN REF. 5).
Y -> I (IN REF. 1).
PT -> GS (IN REF. 1).
PT -> CR (IN REF. 1).
PL -> LA (IN REF. 1).
PHHSSEHISSASSRMESAIHASSSNSEGFRYSKAGARISG
                                                                                                                                                                                                                                                                                                INPTERVIE -> SLAQQRTYIVSQFEDAGVGYNMPAAAIL
EGPLDIQKLERAFQGLIRRHESLR (IN REF. 1).
VC -> DS (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                             V. -> US (IN REF. 1).

L -> V (IN REF. 1).

T -> S (IN REF. 1).

T -> S (IN REF. 1).

A -> R (IN REF. 1).

PAVFIQMD -> LRCLSKWT (IN REF. 1).

PAVFIQMD -> LRCLSKWT (IN REF. 1).

P -> L (IN REF. 1).

R -> QQ (IN REF. 1).

C -> S (IN REF. 1).

C -> S (IN REF. 1).

M. SSING (IN REF. 1).

AV -> RC (IN REF. 1).

AT -> SP (IN REF. 1).
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-!- FUNCTION. Unusual circulary permuted GTPase that catalyzes rapid hydrolysis of GTP with a slow catalytic turnover (By similarity).
-!- SUBUNIT: Monomer (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1; Length 3588;
Pred. No. 62;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3588 AA; 402072 MW; BC02FB157D7F1FDB CRC64;
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PH -> GQ (IN REF. 1).
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Probable GTPase engC (EC 3.6.1.-).
ENGC OR BH2503.
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STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; Pubmed=11058132;
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15-MAR-2004 (Rel. 43, Last sem
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TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT IN THE DEVELOPING LIMB BUD EPITHELIUM DURING TI PIONEER AXON OUTGROWTH.

SIMILARITY: Belongs to the semaphorin family.

SIMILARITY: Contains 1 Sema domain.

SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isbister C.M., Tsai A., Wong S.T., Kolodkin A.L., O'Connor T.D., "Discrete roles for secreted and transmembrane semaphorins in neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth cone guidance in vivo.",
Development 126:2007-2019(1999).
-!- FUNCTION: ACTS AS CHEMOREDISTURE GUIDANCE MOLECULE CRITICAL FOR
AXON FASCICULATION AND FOR DETERMINING BOTH THE INITIAL DIRECTION
AND SUBSEQUENT PATHFINDING EVENTS OF THE II AXON PROJECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Neoptera; Orthopteroidea; Orthoptera, Caelifera, Acridomorpha,
Acridoidea; Acrididae, Cyrtacanthacridinae; Schistocerca.
                                                                                                                                                                                                                                                                                                                      ENGC GTPASE.
GTP (PROBABLE).
GTP (PROBABLE).
GTP (PROBABLE).
KNUCKLE-LIKE CYSTEINE CLUSTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 1; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  7DC80C97AFA93A9B CRC64;
SIMILARITY: Contains 1 engC GTPase domain.
                                                                                                                                                                     EMBL, AP001515; BAB06222.1; -
PIR, G83962; G83962.
HAMAP; MF 01820; -; J.
InterPro; IPR004081; DUF258.
Pfam; PF03193; DUF258, 1.
TIGRPAMS; TIGR00157; TIGR00157; 1.
PROSITE; PS50936; ENGC_GTPASE; 1.
Hydrolase; GTP-binding; Complete proteome.
DOMAIN 72 221 ENGC GTPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-CCT-2003 (Rel. 42, Last annotation update)
Semaphorin 2A precursor (Sema 2A) (Sema II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 8.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                  33449 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 46.2'
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294 AA;
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InterPro; IPR00110; Ig-like.
InterPro; IPR001529; Ig.
InterPro; IPR001627; Sema:
Pfam; PF01403; Sema: 1.
SWART; SW006409; IG; 1.
SWART; SW00630; Sema: 1.
SWART; SR00630; Sema: 1.
SWART; IRRUPART; SW00610; IG IIRE; 1.
Signal; IRRUPART                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..) (POTENTIAL).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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101-FEB-1994 (Rel. 28, Last Sequence update)
101-FUL-1998 (Rel. 36, Last annotation update)
Olfactory receptor 7A (K18) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 19; ; Mismatches
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Best Local Similarity 43.8
Matches 7; Conservative
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SIGNAL
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EMBL; L14568; AAA39852.1; -.

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SGD; S0003406; CBP4.
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 ;
 "Characterization of CBP4, a new gene essential for the expression of ubiquinol-cytochrome c reductase in Saccharomyces cerevisiae."; J. Biol. Chem. 269:21284-21292(1994).
 Gaps
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 ..
 MGD; MGI:104712; Olfr7.
InterPro; IPR0002205, GPRR_Rhodpsn.
PFEM; PF00011; Thm 1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PARTIAL.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_Protein coupled receptor; Transmembrane; Multigene family; Olfaction.
 Score 39; DB 1; Length 161;
Pred. No. 7;
 3; Indels
 CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
 17562 MW; 7A5140BB1EFB7FB7 CRC64;
 Saccharomycetales, Saccharomycetaceae, Saccharomyces.
NCBI_TaxID=4932;
 01-OCT-1994 (Rel. 30, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
EBP4 protein, mitochondrial precursor.
CBP4 OR YGR174C.
 170 AA
 1; Mismatches
 Saccharomyces cerevisiae (Baker's yeast).
 PRT;
 SEQUENCE FROM N.A.
MEDLINE=94342301; PubMed=8063753;
 EMBL; Z72959; CAA97200.1; -. PIR; S64488; S64488. GermOnline; 141486; -.
 EMBL; U10700; AAA61566.1; -.
 47.08;
 66.7%;
 8; Conservative
 5 ickprivkvims 16
 3 IAKOMTYKVYMS 14
 STANDARD;
 1
18
37
75
98
115
139
151
151
 116 1
140 1
152 >1
161 1
 PIR; A40745; A40745
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 Crivellone M.D.;
 MEMBRANE
 CBP4 YEAST
 NON TER
DOMAIN
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CBP4_YEAST
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 ..
0
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 Complete proteome
 Gaps
 Gaps
 Ж,
 Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Garbam D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
 ..
 .,
 FUNCTION: Not known, probably involved in fatty acid or phospholipid synthesis (By similarity). SIMILARITY: Belongs to the plsx family.
 Length 170;
 Length 337;
 Indels
 Indels
 Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
 MITOCHONDRION (POTENTIAL).
CBP4 PROTEIN.
S -> F (IN REF. 1).
 Fatty acid biosynthesis; Phospholipid biosynthesis; Cor
SEQUENCE 337 AA; 36266 MW; C6E51574FA15D508 CRC64;
 D88F92EADF0B366E CRC64;
 3;
 Fatty acid/phospholipid synthesis protein plsx
PLSX OR AQ_1101.
 Score 39; DB 1;
Pred. No. 14;
4; Mismatches
 47.0%; Score 39; DB 1; 61.5%; Pred. No. 7.3;
 (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
 368 AA.
 337 AA
 2; Mismatches
 SERC NEIMA STANDARD; PRT; 36: 034370; 033382; 033383; 033384; 033386;
 HAMAP, WE 00019; -; 1.
InterPro: IPR003664; FA synthesis.
Pfan, PP02504; FA synthesis, 1.
ProDom; PD006974; FA synthesis; 1.
IIGRFAMS; TIGR00182; Pl8X; 1.
 MEDLINE=98196666; PubMed=9537320;
Mitochondrion; Transit peptide.
 EMBL; AE000723; AAC07145.1; -. PIR; G70394; G70394.
 170 AA; 20219 MW;
 47.0%;
 50.0%;
 Nature 392:353-358(1998).
 1 SVIAKOMTYKVYM 13
 10 AVIAKOROYKHYL 22
 8; Conservative
 STANDARD;
 Conservative
 4 AKOMTYKVYMSG 15
 ||:: ||:|: |
26 AKELGYKIYLVG 37
 170
 65
 Query Match
Best Local Similarity
 Local Similarity
 SEQUENCE FROM N.A.
 Aquifex aeolicus.
 65
 30-MAY-2000
 30-MAY-2000
 28-FEB-2003
 9
 PLSX AQUAE
 aeolicus."
 CONFLICT
 SEQUENCE
 Query Match
 TRANSIT
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 % PIR; F81816; F816...

R HSSP; PS2721; 1BJN.

JR HAMAP; ME 00160; -; 1.

DR InterPro; IPR000192; Aminotrans V.

DR InterPro; IPR000184; Pser aminitransf.

DR Probom; P0001544; Pser aminitransf.

DR PROSITE; PS00555; AA TRANSFER CLASS 5; 1.

DR PROSITE; PS00555; AA TRANSFER CLASS 5; 1.

KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;

KW Aminotransferase; Pyridoxine biosynthesis; Complete proteome.

TNDING 203 203 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

TNDING 168 168 R. C. (IN STRAIN B293, Z3910 AND 23918).

-- S (IN STRAIN B293, Z3524, Z3910,
 Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., "Complete DNA Sequence of a serogroup A strain of Neisseria
 -!- CORACTOR: Pyridoxal phosphate.
-!- PATHWAY: Required both in major phosphorylated pathway of serine biosynthesis and in the biosynthesis of pyridoxine.
-!- SUBCELULLAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent
 STRAIN=Various strains; MEDINE=9350862; MEDINE=98010345; PubMed=9350862; Morelli G., Malorny B., Mueller K., Seiler A., Wang J.-F., Morelli G., Achtman M.; "Clonal descent and microevolution of Neisseria meningitidis during
 Nature 404:502-506 (2000).
-!- CATALYTIC ACTIVITY: O-phospho-L-serine + 2-oxoglutarate = 3-
phosphonooxypyruvate + L-glutamate.
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
15-DEC-1998 (Rel. 37, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoserine aminotransferase (EC 2.6.1.52) (PSAT).
SERC OR NMA1894.
 STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919;
 Neisseria meningitidis (serogroup A)
 30 years of epidemic spread."; Mol. Microbiol. 25:1047-1064(1997).
 EMBL, AF004820, AAC32675.1; --
EMBL, AF004821, AAC32679.1; --
EMBL, AF004823, AAC32683.1; --
EMBL, AF004823, AAC32691.1; --
EMBL, AF004824, AAC32691.1; --
EMBL, AF004825, AAC32695.1; --
EMBL, AF004825, AAC32699.1; --
EMBL, AL162757, CAB85115.1; --
PRR, F81816, F81816.
 Neisseriaceae, Neisseria.
NCBI_TaxID=65699;
 aminotransferases.
 [2]
SEQUENCE FROM N.A.
 meningitidis Z2491
 SEQUENCE FROM N.A.
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 MEDLINE=20175755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B strain
 Gaps
 Science 287:1809-1815(2000).

-!- CATALYTIC ACTIVITY: O-phospho-L-serine + 2-oxoglutarate = 3-phosphonoxypyruvate + L-glutamate.

-!- COPACTOR: Pyridoxal phosphate.
-!- COPACTOR: Pyridoxal phosphorphated pathway of serine blosynthesis and in the blosynthesis of pyridoxine.
-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent aminotransferases.
240 D -> E (IN STRAINS Z3915 AND Z3524).
289 G -> D (IN STRAINS B293, Z3910 AND Z3918).
T3918).
T -> S (IN STRAIN Z4296).
41388 MW, 3D3E305853698537 CRC64;
 ;
0
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
 47.0%; Score 39; DB 1; Length 368; 70.0%; Pred. No. 16;
 ProDom, PD001544; Pser_amintransf; 1.
TIGRFAMS; TIGR01364; serC_1; 1.
PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.
Serine biosynthesis; Pyridoxine biosynthesis; Transferase; Aminotransferase; Pyridoxal phosphate; Complete proteome.
 16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoserine aminotransferase (BC 2.6.1.52)
 Pred. No. 16;
1; Mismatches
 or send an email to license@isb-sib.ch).
 HAWAP; MF_00160; -; 1.
InterPro; IPR001923, Aminotrans_V.
InterPro; IPR003248; Pser_amintransf.
Pfam; PF00266; aminotran_5; 1.
 Neisseria meningitidis (serogroup B)
 EMBL; AE002514; AAF41989.1; -.
 16-OCT-2001 (Rel. 40, Created)
 / Serogroup B;
 Query Match
Best Local Similarity 70.0
Matches 7; Conservative
 STANDARD;
 248 TYAIYMSGLV 257
 336
 8 TYKVYMSGTV 17
 PIR; H81059; H81059.
 368 AA;
 HSSP; P23721; 1BJN.
 [1]
SEQUENCE FROM N.A.
 SERC OR NMB1640.
 NCBI_TaxID=491;
 STRAIN=MC58
 SERC NEIMB
 SEQUENCE
 VARIANT
VARIANT
 VARIANT
 P57007
 SERC NEIMB
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PIR; A38531; YGCEVC.
HSSP; P14687; 1AMU.
 domains."
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=5044;
 (Potential)
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 functional
 CEPAC
 InterPro;
InterPro;
 P25464;
 ACVS
 Matches
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 .
 -!- FUNCTION: Involved in microtubule organization by the microtubule organizing centre, the spindle pole body (SPB). Probably part of the microtubule attachment site at the SPB.
-!- SUBCULI: Interacts with TUB4 and SPC97.
-!- SUBCELLUIAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the GCP family.
 Geissler S., Pereira G., Spang A., Knop M., Soues S., Kilmartin J.V., Schiebel E.,
 Gaps
 "The spindle pole body component Spc98p interacts with the gamma-tubulin-like Tub4p of Saccharomyces cerevisiae at the sites of microtubule attachment."; microtubule attachment."; EMBO J. 16:3899-3911(1996).
 'n.
 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
SprEB-2003 (Rel. 41, Last annotation update)
Spindle pole body component SPC98.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycota, Saccharomyceties;
Saccharomycetales; Saccharomycetes.
 Mallet L., Bussereau F., Jacquet M.;
"A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,
MEP2, CAP/SRV2, NAM9, FKE1/FPR1/FBP1, MOM22 and CPT1, predicts a
adenosine deaminase gene and 14 new open reading frames.";
Yeast 11:1195-1209(1995).
 de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pandolfo Pallavicini A., Lanfranchi G., Valle G.;
"The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces cerevisiae reveals an unusually high number of overlapping open reading frames.";
Yeast 13:261-266(1997).
PYRIDOXAL PHOSPHATE (BY SIMILARITY)
 ö
 Length 368;
 2; Indels
 97DFCE52BBE5E021 CRC64;
 Score 39; DB 1;
Pred. No. 16;
 Mismatches
 PRT;
 CHARACTERIZATION.
MEDLINE=96324398; PubMed=8670895;
 MEDLINE=97245296; PubMed=9090055;
 MEDLINE=96109932; PubMed=8619318;
 EMBL; Z46843; CAA86899.1; -.
EMBL; Z69382; CAA93378.1; -.
EMBL; Z71402; CAA96007.1; -.
PIR; S59262; S59262.
GermOnline; 143132; -.
SGD; S0005070; SPC98.
 41393 MW;
 47.08;
 70.0%;
 Conservative
 STANDARD;
 248 TYAIYMSGLV 257
 8 TYKVYMSGTV 17
 Query Match
Best Local Similarity
7; Conserve
 368 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=4932;
 STRAIN-S288C;
 SP98_YEAST
ID SP98_YEAST
 Schiebel
 SEQUENCE
 BINDING
 P53540;
```

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GO; GO:0005822; C:inner plaque of spindle pole body; IDA.
GO; GO:0005824; C:outer plaque of spindle pole body; IDA.
GO; GO:000520; F:structural constituent of cytoskeleton; IPI.
GO; GO:0007020; F:structural constituent of cytoskeleton; IPI.
GO; GO:000071; P:microtubule nucleation; IPI.
GO; GO:000071; P:microtubule nucleation; IPI.
InterPro; IRR007259; Spc97.
Spc97.
Spc97.
Spc97.
Microtubule; Nuclear protein.
SRQUENCE 846 AA; 98226 MW; 803048B05D5E5105 CRC64;
 Cephalosporium acremonium (Acremonium chrysogenum).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; mitosporic Hypocreaceae;
 intermediates.
-!- CATALYTIC ACTIVITY: L-2-aminohexanedioate + L-cysteine + L-valine + A ATP = N-[L-5-amino-5-carboxypentanoyl]-L-cysteinyl-D-valine + 3 AMP + 3 diphosphate.
-!- COFACTOR: Contains 3 covalently bound phosphopantetheines
 cluster
 STRAIN=ATCC 11550; MEDLINE=91168300; PubMed=2076552; Hoskins J.A., O'Callaghan N., Queener S.W., Cantwell C.A., Wood J.S., Chen V.J., Skatrud P.L.; "Gene disruption of the pcbAB gene encoding ACV synthetase in
 -!- PATHWAY: Biosynthesis of penicillin and cephalosporin; first step
 Gaps
 Curr. Genet. 18:523-530(1990).
-!- FUNCTION: Each of the constituent amino acids of the tripeptide acv are activated as aminoacyl-adenylates with peptide bonds formed through the participation of amino acid thiolester
 Gutierrez S., Diez B., Montenegro B., Martin J.F.; Gutierrez S., Diez B., Montenegro B., Martin J.F.; Characterization of the Cephalosporium acremonium pcbAB gene moroding alpha-aminoadipyl-cysteinyl-valine synthetase, a large multidomain peptide synthetaes: linkage to the pcbC gene as a clust of early cephalosporin biosynthetic genes and evidence of multiple
 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase
(EC 6.3.2.26) (Delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine
synthetase) (ACV synthetase) (ACVS).
 -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
 .;
0
 Score 39; DB 1; Length 846; Pred. No. 35; 4; Mismatches 3; Indels
 PARTIAL SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 -!- SIMILARITY: Contains 3 acyl carrier domains
 PRT; 3712 AA
 Bacteriol. 173:2354-2365(1991).
 MEDLINE=91177827; PubMed=1706706;
 IPR001242; Condensatn.
IPR006163; Pp_bind.
IPR006162; Ppantne_S.
 InterPro; IPR000873; AMP-bind.
InterPro; IPR001242; Condensat
InterPro; IPR006163; Pp_bind.
 47.0%;
 394 IPKELAYKIFMIG 406
 Cephalosporium acremonium.
 3 IAKQMTYKVYMSG 15
 Conservative
 STANDARD;
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us-09-890-463-2.rsp

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Matches
 SHAMMETERS
 δ
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 ö
 Klenk H.-P., Clayfon R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Kirkness B.F., Googne J.D., Weidman J.F., McDonald L., Utterback R.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Wason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 Gaps
 "The complete genome sequence of the hyperthermophilic, sulphate-
 PHOSPHOPANTETHEINE (BY SIMILARITY)
 PHOSPHOPANTETHEINE (BY SIMILARITY)
PHOSPHOPANTETHEINE (BY SIMILARITY)
FRANCE (BY SIMILARITY)
THIOESTERASE (BY SIMILARITY).
414767 MM; 4EE3C1EBSEBEF9B7 CRC64;
 -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
 .
0
R InterPro; IPR000379; Ser estrs.
R InterPro; IPR001031; Thioseterase.
R Ffam; PF005601; AMP-binding; 3.
R Pfam; PF00568; Condensation; 3.
R Pfam; PF00550; pp-binding; 3.
R Pfam; PF00154; AMPBINDING; 3.
R PROSITE; PS00015; PHOSPHORNTETHBINE; 2.
R PROSITE; PS000455; AMP BINDING; 3.
R PROSITE; PS0075; ACF DOMAIN; 3.
R Ligase; Antibiotic biosynthesis; Multifunctional enzyme; Repeat; Phosphopantetheine.
REPEAT 234 1062 DOMAIN 1 (ADIPATE_ACTIVATING).
 DOMAIN 1 (ADIPATE-ACTIVATING).
DOMAIN 2 (CYSTEINE-ACTIVATING)
DOMAIN 3 (VALINE-ACTIVATING).
 Length 3712;
 4; Indels
 Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
 ACYL CARRIER (ACP) 1.
ACYL CARRIER (ACP) 2.
ACYL CARRIER (ACP) 3.
 Score 39; DB 1; L
Pred. No. 1.5e+02;
}; Mismatches 4;
 (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
 ng archaeon Archaeoglobus fulgidus.";
390:364-370(1997).
 SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
 PRT;
 47.0%;
 Hypothetical protein AF1562.
 414 SKOLAYVTYTSGT 426
 4 AKOMTYKVYMSGT 16
 Conservative
 STANDARD;
 Archaeoglobus fulgidus.
 1953
3027
827
 Query Match
Best Local Similarity
7, Conserva
 3712 AA;
 NCBI_TaxID=2234;
 827
1916
2990
3568
 L6-OCT-2001
 16-OCT-2001
16-OCT-2001
 YF62 ARCFU
028710;
 ACT SITE
SEQUENCE
 reducing
 BINDING
 BINDING
 DOMAIN
 Nature
 REPEAT
 REPEAT
 DOMAIN
 AF1562
 임
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0
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
 MEDINE=94049112; PubMed=8221804;
MEDINE=94049112; PubMed=8221804;
Lindquist S., Weston-Hafer K., Schmidt H., Pul C., Korfmann G.,
Erickson J., Sanders C., Martin H.H., Normark S.;
"AmpG, a signal transducer in chromosomal beta-lactamase induction.";
Mol. Microbiol. 9:703-715(1993).
 SEQUENCE FROM N.A.

STRAIN=O6:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland U. Dunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Molley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:1702.71024(2002)
 Gaps
 -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregot J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
 Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
 .;
 DB 1; Length 140;
 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
 Complete proteome
 140 AA; 15667 MW; 937DCB5585A17991 CRC64;
 YAJG ECOLI STANDARD; PRT; 192 AA. P3671; P77210; 01-UUN-1994 (Rel. 29) Last sequence update) 01-UUN-1994 (Rel. 29) Last sequence update) 10-OCT-2003 (Rel. 29, Last annotation update) Hypothetical lipoprotein yajG precursor. YAJG OR BO434 OR E0546. Escherichia coli, and Escherichia coli 06.
 Pred. No. 9.3;
; Mismatches
 45.8%; Score 38;
 (Probable).
 Hypothetical protein; Transmembrane; Co
TRANSMEM 20 42 POTENTIAL
 POTENTIAL
 POTENTIAL.
 9
 Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992;
 Similarity 37.5%;
6; Conservative
 2 VIAKQMTYKVYMSGTV 17
 29 IIFMAITFAIYVSGTL 44
EMBL; AE000994; AAB89687.1;
 42
 PIR; A69445; A69445.
TIGR; AF1562; -.
 STRAIN=K12 / MG1655;
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 TRANSMEM
SEQUENCE
 TRANSMEM
 Query Match
 RESULT 14
YAJG_ECOLI
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 Gaps
 MEDLINE=84259352; PubMed=6744416;
Youvan D.C., Bylina E.C., Alberti M., Begusch H., Hearst J.E.;
"Mucleotide and deduced polypeptide sequences of the photosynthetic
reaction-center, B870 and tenna, and flanking polypeptides from R.
 HYPOTHETICAL LIPOPROTEIN YAJG.
N-palmitcyl cysteine (Potential).
S-diacylglycerol cysteine (Potential).
9E9E6568E9253451 CRC64;
 STRAIN=SB1003 / CB1029;
BDDILNRE-203798964: PubMed=10811655;
FUJita Y., Bauer C.B.; "Reconstitution of light-independent protochlorophyllide reductase
 01-WAY-1992 (Rel. 22, Created)
01-WAY-1992 (Rel. 22, Last sequence update)
88-FEB-2003 (Rel. 41, Last annotation update)
Light-independent protocollorophyllide reductase iron-sulfur ATP-
binding protein (EC 1.18.-.-) (LI-POR subunit L) (DPOR subunit L
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
 0
 MEDLINE=90368852; PubMed=2203738;
Yang Z., Bauer C.E.;
"Rhodbacter capsulatus genes involved in early steps of the bacteriochlorophyll biosynthetic pathway.";
J. Bacteriol. 172:5001-5010(1990).
 Score 38; DB 1; Length 192;
Pred. No. 13;
 4; Indels
 SEQUENCE FROM N.A.
STRAIN=SBB1003 / St Louis;
Burke D.H., Alberti M., Armstrong G.A., Hearst J.E.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
 EcoGene, EG12182; yajg.
InterPro; IPR005619; Lipoprotein 16.
InterPro; IPR00437; Prok lipoprote 5.
Pram; PR0323; Lipoprotein 16; 1.
ProDom; PD036382; Lipoprotein 16; 1.
PROSITE; PS00013; PR00AR LIPOPROTEIN; 1.
Hypothetical protein; Membrane; Lipoprotein; Signal; Complete proteome; Palmitate.
 Rhodobacter capsulatus (Rhodopseudomonas capsulata)
 304 AA
 2; Mismatches
 POTENTIAL.
 EMBL, 867816; AAB28883.2; -- BMBL, AEO00149; AAC1337.1; ALT INIT. EMBL; U82664; AAB40190.1; ALT INIT. EMBL; AE016756; AAN79024.1; ALT INIT.
 PRT;
 18 192 HY
18 18 N-1
18 18 S-1
192 AA; 20950 MW;
 PRELIMINARY SEQUENCE FROM N.A.
 45.8%;
 |: |||| : || |
83 VLEKQMTARGYMVG 96
 2 VIAKQMTYKVYMSG 15
 8; Conservative
 STANDARD;
 Cell 37:949-957(1984).
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 CHARACTERIZATION
 NCBI_TaxID=1061;
 BCHL_RHOCA
P26237;
 capsulata.
 SEQUENCE
 SIGNAL
 RESULT 15
BCHL_RHOCA
 LIPID
 Matches
 엄
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 ·.
 -!- FUNCTION: Uses Mg-ATP and reduced ferredoxin to reduce ring D of protochlorophyllide (Pchlide) to form chlorophyllide a (Chlide). This reaction is light-independent.
-!- PATHWAY: Light-independent bacteriochlorophyll biosynthesis.
-!- SUBUNIT: Protochlorophyllide reductase is thought to be composed of three subunits; bchL, bchN and bchB. Homodimer of bchL subunit
 Gaps
from purified bchL and bchN-bchB subunits. In vitro confirmation of
 PROSID: PROFESSIONAL ALTHOUGH PROPERTY ATP-binding; Iron-sulfur; 4Fe-48.

ATP-binding; Iron-sulfur; 4Fe-48.

ATP (POTENTIAL).

METAL 131 131 131 131 131 131 130N-SULFUR (4FE-48) (BY SIMILARITY)

METAL 165 165 187 SIMILARITY)
 nitrogenase-like features of a bacteriochlorophyll biosynthesis
 ..
0
 45.8%; Score 38; DB 1; Length 304; 47.1%; Pred. No. 20;
 (By similarity).
-!- SIMILARITY: Belongs to the nifH / bchL / chlL family.
 5; Indels
 3A49C39BCF15AECC CRC64;
 Mismatches
 EMBL; M34843; AAA26098.1; --
EMBL; Z1165; CAA77523.1; --
EMBL; K01183; --
EMR, B36716; B36716.
PIR; H28771; H28771.
HARAP; MF 00355; --
INTERPO; IPR00392; NITROGENASEII.
INTERPO; IPR00392; NITROGENASEII.
PRINTS; PR0091; NITROGNASEII.
TIGRAMA; TIGROLAS! NITROGNASEII.
TIGRAMA; TIGROLAS! NITROGNASEII.
TIGRAMS; TIGROLAS! NITROGNASEII.
PROSITE; PS00746; NIFH FRXC_1; 1.
PROSITE; PS00746; NIFH FRXC_2; 1.
 Search completed: August 12, 2004, 06:20:06
 Biol. Chem. 275:23583-23588(2000).
 Fujita Y ;
Unpublished observations (JUL-2001)
 131 131 II
165 165 II
304 AA; 33204 MW;
 198 AVQAKSVNYKVRLAGCV 214
 1 SVIAKOMTYKVYMSGTV 17
 8; Conservative
 Local Similarity
 Job time : 3.04508 secs
 CHARACTERIZATION.
 SEQUENCE
 Query Match
 enzyme
 ò
 셤
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Goniopora tenuidens.
 47.0
47.0
47.0
 Q95P04;
 Q95P04
 RESULT 1
 RESULT 2
 Q95P04
 Q97LU2
 ð
 Q95p04 goniopora to Q97lu2 clostridium Q8xipl clostridium Q8wipl clostridium Q86wil homo sapien Q86wil homo sapien Q8mu45 condylactis Q95wl condylactis Q95wl condylactis Q95wj sulfolobus Q96yj sulfolobus Q96yj lactococus Q9cif lactococus Q9xko bacillus ha
 August 12, 2004, 06:12:47; Search time 4.42418 Seconds (without alignments) 1212.385 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Description
 1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
 Total number of hits satisfying chosen parameters:
 1017041 segs, 315518202 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 Q96YI5
Q45675
Q9CI65
 Q95P04
Q97LU2
Q8XIP1
Q9UF27
 Q97FT4
Q7XDZ1
Q9KBK0
 Q8MU45
Q95W11
 sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
 Q95W86
 Q9U6Y8
 09GTJ7
 Gapop 10.0 , Gapext 0.5
 Q86WI1
 sp_fungi:*
sp_human:*
sp_invextebrate:*
sp_mhc:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
 1 SVIAKOMTYKVYMSGTV 17
 sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 sp_archea:*
sp_bacteria:*
sp_fungi:*
 Minimum DB seq length: 0 Maximum DB seq length: 2000000000
 110
110
110
 Query
Match Length DB
 US-09-890-463-2
 SPTREMBL 25:*
 BLOSUM62
 10:
 Scoring table:
 Perfect score:
 Score
 Sequence:
 Searched:
 Database
 Run on:
 Title:
```

```
17 40 48.2 294 16 Q9K921 Q98BM2 D98C1 bacillus ha Q88BM2 19 40 48.2 557 16 Q88M2 Q88BM2 Q88BM2 D98CC1 anabidopsis Q88CC1 40 48.2 1086 16 Q8KVC1 Q88CC2 Q88CC2 anabaena sp. 21 40 48.2 1086 16 Q8KVC1 Q84CC anabaena sp. 22 39 47.0 150 2 Q9K2Y3 G952C3 anabidopsis A7.0 150 2 Q5461 G952C3 anabidopsis G952C3 anabidopsis G952C3 39 47.0 150 2 Q5461 G952C3 anabidopsis G952C3 anabidopsis G952C3 39 47.0 150 2 Q5463 G952C3 anabisocria m Q52C4C3 G952C3 anabidopsis G952C3 39 47.0 150 2 Q52C4C3 G952C3 G952C3 anabidopsis G952C3 G952
```

### ALIGNMENTS

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19504

10404

105504

10704

108504

108504

108504

108504

108504

108504

109504

109504

101-DEC-2001 (TrEMBLrel. 19, Last sequence update)

101-DEC-2003 (TrEMBLrel. 25, Last annotation update)

101-OCT-2003 (TrEMBLrel. 25, Last annotation update)

101-OCT-2003 (TrEMBLrel. 25, Last annotation update)

101-OCT-2003 (TrEMBLrel. 25, Last annotation update)

102-OCT-2003 (TrEMBLrel. 25, Last annotation update)

103-OCT-2003 (TrEMBLrel. 25, Last annotation update)

104-OCT-2003 (TrEMBLrel. 25, Last annotation update)

105-OCT-2003 (TrEMBLrel. 25, Last annotation update)

106-OCT-2003 (TrEMBLrel. 25, Last annotation update)

107-OCT-2003 (TrEMBLrel. 25, Last annotation update)

10850-OCT-2003 (TrEMBLrel. 2501)

1087-OCT-2003 (TrEMBLrel. 2601)

1087-OCT-2003 (TrEMBLrel. 2003)

1087-OC
```

.; 0 424 AA

```
TISSUE-Uterus;
Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133640; CAB63761.1; -.
PIR; T43498; T43498.
Hypothetical protein.
1
 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 51.8%; Score 43; DB 4; Length 424; 43.8%; Pred. No. 34; ive 5; Mismatches 4; Indels
 424 AA; 46402 MW; 35523FD7C62313A2 CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Fragment).
PRT;
 Hum. Mol. Genet. 12:685-698(2003).
EMBL, AY219181; AAO60072.1; -
InterPro; IPR00110; Ig-like.
InterPro; IPR002909; IPT TIG.
InterPro; IPR006626; PbHI.
 3835
 16
 1 SVIAKOMTYKVYMSGT 16
 1 SIVALNKSYEVYFTGT 16
 | :: | :| :| | SIVALNKSYEVYFTGT
 1 SVIAKOMTYKVYMSGT
 Query Match
Best Local Similarity 43.0.
Tr Conservative
 Conservative
 PRELIMINARY;
PRELIMINARY;
 Pfam; PF01833; TIG; 14.
 Homo sapiens (Human).
 Homo sapiens (Human)
 Local Similarity
es 7; Conserv
 SEQUENCE FROM N.A.
 NCBI TaxID=9606;
 NCBI_TaxID=9606;
 Fibrocystin L.
 SEQUENCE
 3820
 Query Match
 Q86WI1
Q86WI1;
 Matches
 RESULT 5
 Q86WI1
ò
 ACCOORDING THE REPORT OF THE T
 g
 .
0
 0
 Noelling J., Breton G., Chelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
D. Bacteriol. 183:4823-4838(2001).

EMBL, AE007561; AAK78442.1;
PIR: G36956; G36956.

Complete proteome.
 Gaps
 Gaps
 Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
 Clostridium perfringens.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
 Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
 ò.
 ö
 54.2%; Score 45; DB 16; Length 398; 47.1%; Pred. No. 14; 7; Indels iive 2; Mismatches 7; Indels
 51.8%; Score 43; DB 16; Length 389; 41.2%; Pred. No. 32;
 6; Indels
 Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP003192; BAB61780.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE. 389 AA; 43138 MW; 36E1230CC603E7CS CRC64;
 398 AA; 45650 MW; 59324A21CA466DFC CRC64;
 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Protein of short-chain alcohol dehydrogenase family
 01-WAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CPE2074.
 389 AA
 Mismatches
 SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
 (TrEMBLrel. 18, Created)
 PRT;
 SEQUENCE FROM N.A.
STRAIN=13 / Type A;
MEDLINE=21664373; PubMed=11792842;
 2;
 4,
 | | ::|| :| ||:
223 SYIGPEVTYPIYREGTI 239
 224 SYIGSPRTYKIYREGTI 240
 1 SVIAKOMTYKVYMSGTV 17
 1 SVIAKQMTYKVYMSGTV 17
 Clostridium acetobutylicum
 Best Local Similarity 41.29
Matches 7; Conservative
 8; Conservative
 PRELIMINARY;
PRELIMINARY;
 Query Match
Best Local Similarity
 Clostridium.
NCBI_TaxID=1502;
 NCBI_TaxID=1488;
 flesh-eater."
 QBXIP1;
01-MAR-2002 (
01-MAR-2002 (
 01-OCT-2001
01-OCT-2001
 SECUENCE
 Query Match
 CAC0462
 QBXIP1
 Matches
 RESULT 3
008XIP1
1D AC 08XIP1
DT 01-M
DT 01-J

 RESULT
09UF27
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8

.; 0

Gaps

.. 0

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0
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 Harris P.C.; a homolog of the autosomal recessive polycystic kidney disease gene, encodes a receptor with inducible I lymphocyte
 .;
0
 SEQUENCE FROM N.A.
MEDLINE=22508206; PubMed=12620974;
Hogan M.C., Griffin M.D., Rossetti S., Torres V.E., Ward C.J.,
 51.8%; Score 43; DB 4; Length 4243; 43.8%; Pred. No. 3.6e+02; ive 5; Mismatches 4; Indels
 PIGHM; SWOOT10; PDH; 14.
SWART; SWOO710; PDH1; 10.
POINTENER 4243 AA; 465745 MW; 36FE9DE63F4931E7 CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 227 AA.
PRT; 4243 AA
 PRT;
 PRELIMINARY;
 RESULT 6
QBMU45
ID QBMU45
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à

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Hypothetical protein, Complete proteome.
SEQUENCE 592 AA, 65796 MW; 3CED613D9A0EB7ED CRC64;
 PRT;
 SEQUENCE FROM N.A. MEDLINE=21538626; PubMed=11682051;
 4;
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 2 VIAKOMTYKVYMSGTV 17
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 GFP-like chromoprotein.
 STRAIN=JCM 10545 / 7;
 Sulfolobus tokodaii
 SEQUENCE FROM N.A.
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 proteins (1).
 Q96YI5
 RESULT 9
 Q96YI5
 δ
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 0
 Gaps
 Gaps
 MEDLINE-21538626; PubMed-11682051;
Gurskaya N.G., Fradkov A.F., Terskikh A., Matz M.V., Labas Y.A.,
Martynov V.I., Yanushevich Y.G., Lukyanov K.A., Lukyanov S.A.;
"GPP-like chromoproteins as a source of far-red fluorescent
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-COT-2003 (TrEMBLrel. 25, Last annotation update)
GFP-like chromoprotein.
Grodylactis passifilora.
Bukaryota; Metazoa; Cindaria; Anthozoa; Zoantharia; Actiniaria; Nymantheae; Actinidae; Condylactis.
 Bukaryota; Metazoa; Cnidaria; Authozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Condylactis.
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 Matz M.V., Lukyanov S.A.;
"Diversity and evolution of GFP-like fluorescent proteins.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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 EMEL, AY037777, AAK71343.1, -.
GO, GO:0006091, P:energy pathways; IEA.
InterPro; IPR009017, GFP like.
InterPro; IPR000786, Green_fl_protein.
Probom; PP013756, Green_fl_protein, 1.
SEQUENCE 227 AA; 25384 MW; D3C6B02F490F3D21 CRC64;
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InterPro; IPR000786; Green_fl_protein.
Pfam; PF01353; GFP; 1.
ProDom; PD013756; Green_fl_protein; 1.
SEQUENCE 227 AA; 25446 MW; E51CC017108593E3 CRC64;
 01-0cT-2002 (TrEMBLrel. 22, Created)
01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein-like protein.
Condylactis gigantea (Giant anemone).
 227 AA.
 227 AA
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 4 LLKESMRIKIYMEGTV 19
 2 VIAKOMTYKVYMSGTV 17
 4 LLKESMRIKIYMEGTV 19
 proteins(1).";
FEBS Lett. 507:16-20(2001).
 Best_Local Similarity 43.8
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 295W11;
 095W86
 Q95W11
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RESULT 095W11

δ

Matches

RESULT 8

Q95W86

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Sulfolobus.
NCBL_TaxID=111955;
 Gurskaya N.G., Fradkov A.F., Terskikh A., Matz M.V., Labas Y.A., Martynov V.I., Yanushevich Y.G., Lukyanov K.A., Lukyanov S.A.; "GFP-like chromoproteins as a source of far-red fluorescent
 Condylactis gigantea (Giant anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Condylactis.
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0
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative glucosamine--fructose-6-phosphate aminotransferase.
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ProDom; PD013756; Green fl protein; 1.
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 49.4%; Score 41; DB 5;
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 PEBS Lett. 507:16-20(2001).

EMBL, AF363775, AAL37537.1;

EMBL, AF363775, Penergy pathways; IEA.

InterPro; IPR009017, GFP like.

InterPro; IPR000786; Green_fl_protein.
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SPECIES=L.lactis; STRAIN=IL1403;
 2683 AVTAENLAYMIYTSGT 2698
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Genome Res. 11:731-753(2001).
49.4%;
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 1 SVIAKOMTYKVYMSGT 16
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 100 KEMTYKFYIS 109
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 5 KOMTYKVYMS
 SEQUENCE FROM N.A.
 Discosoma sp
 Query Match
Best Local
 OSUGY8;
 Q9U6Y8
 Q9C165
 Matches
 RESULT 11
 RESULT 12
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 STEALNEELES TROUGHS,

WEDLINE=93181186; PubMed=8441623;

REDLINE=93181186; PubMed=8441623;

A Funa S., Pujishima Y., Corbell N., D'Souza C., Nakano M.M., Zuber P.,

A Tuma S., Pujishima Y., Corbell N., D'Souza C., Nakano M.M., Zuber P.,

A Tumane K.;

"Nucleotide sequence of 5' portion of srfa that contains the region

Trequired for competence establishment in Bacillus subtilis.";

Nucleic Acids Res. 21:39-97(1993).

EMBL; X72672; CAA51223.1; -.

RESP; Pl4687; lAMU.

RESP; Pl4687; lAMU.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR00162; Pmathabolism; IEA.

InterPro; IPR00162; Ppathne S.

InterPro; IPR00162; Ppathne S.

InterPro; IPR00162; Ppathne S.

InterPro; IPR00162; Ppathne S.

InterPro; IPR00163; AMP-binding; 3.

Rean; PP00501; AMP-binding; 3.

REAm; PR00155; APP-BINDING; 3.

RROSITE; PS00015; APP-BINDING; 3.

RROSITE; PS00015; APP-BINDING; 3.

RWOSITE; PS00015; APP-BINDING; 3.

RWOSITE; PS00015; APP-BINDING; 3.
 'Analysis of errors in finished DNA sequences: the surfactin operon of
 Gaps
 ;
0
 Length 592;
 Fabret C., Quentin Y., Guiseppi A., Busuttil J., Haiech J.,
 > P (IN REF. 2).
> P (IN REF. 2).
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Last annotation update)
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G -> R (IN REF. 2).
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E -> A (IN REF. 2).
L -> A (IN REF. 2).
A -> P (IN REF. 2).
A -> P (IN REF. 2).
A -> D (IN REF. 2).
H -> A (IN REF. 2).
E -> P (IN REF. 2).
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 3; Mismatches
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 Bacillus subtilis as an example.";
Microbiology 141:345-350(1995).
 STRAIN=168 trpC2;
MEDLINE=95219089; PubMed=7704264;
 400937 MW;
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 1 SVIAKOMTYKVYM 13
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 940
1310
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 2070
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 2563
 Surfactin synthetase.
Ouery Match
Best Local Similarity
Tr Conserve
 Phosphopantetheine.
 Bacillus subtilis.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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Q45675;
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 RESULT 10
245675
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SPECIES=L.lactis (subsp. lactis); STRAIN=IL1403;
MEDLINE=2123:186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
 Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;
 Gaps
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360, 1358;
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SPECIES-L.lactis, STRAIN-IL1403;
TRANSPOSON-transposon-like element TnX;
Calero S., Ehrlich S.D., Jamet B., Bolotin A., Renault P.;
"Characterization of the two genes encoding histone-like proteins of the HV family in Lactococcus lactis IL1403.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AE06285; AAK04599.1. -.

EMBL, AF320916; AAK08221.1; -.
 Gaps
 Bolotin A., Mauger S., Malarme K., Ehrlich S.D., Sorokin A.; "Low-redundancy sequencing of the entire Lactococcus lactis IL1403
 ..
 .
0
 Lactococcus lactis (subsp. lactis) (Streptococcus lactis), and Lactococcus lactis.
Length 3583;
 Score 40; DB 16; Length 218; Pred. No. 60;
 5; Indels
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Hypothetical protein; Complete proteome.
SEQUENCE 218 AA; 24616 MW; C38957B3E7A798CB CRC64;
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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 01-MAY-2000 (TrEMBLrel. 13, Created)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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 Antonie Van Leeuwenhoek 76:27-76(1999).
 PRT;
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 PRELIMINARY;
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 STRAIN=cv. Nipponbare;
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 chromosome 10
 DNA-binding.
 152
 SEQUENCE
 Query Match
 Q7XDZ1
 Q97FT4
 RESULT 14
 RESULT 15
 297FT4
 O7XDZ
 ACCOUNT REPORT OF THE REPORT O
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 0;
 Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;
Discosomatidae; Discosoma.
 Gaps
 Gaps
 SEQUENCE FROM N.A.
MEDLINE=99436614; PubMed=10504696;
MAZZ M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G.,
Markelov M.L., Lukyanov S.A.;
"Fluorescent proteins from nonbioluminescent Anthozoa species.";
"At Biotechnol. 17:969-973(1999).
 Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G., Markelov M.L., Lukyanov S.A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF168419; AF703369.1; -.
PDB; 1G7K; 07-NOV-01.
PDB; 1G7K; 06-DEC-00.
 "Novel fluorescent protein from Discosoma coral and its mutants possesses a unique far-red fluorescence."; FEBS Lett. 479:127-130(2000).
EMBL; AF272711; AAG16224.1; -.
 0
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0
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ProDom; PD013756; Green fl protein; 1.
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SEQUENCE 230 AA; 26370 WW; 5215B1B436D67E51 CRC64;
 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
 GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP like.
InterPro; IPR000786; Green_fl_protein.
 PRT;
 1 SVIAKQMTYKVYMSGTV 17
 1 SVIAKOMTYKVYMSGTV 17
 6 NVIKEFMRFKVRMEGTV 22
 Discosoma
 Local Similarity 52.9
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 Red fluorescent protein.
 Discosoma sp. SSAL-2000
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 PF01353; GFP; 1
 Query Match
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Matches 9; Conserv
 NCBI_TaxID=137428;
 SEQUENCE FROM N.A.
Discosomatidae; D. NCBI_TaxID=86600;
 Query Match
 09GTJ7;
 Q9GTJ7
 FP593.
 Best Loca
Matches
 RESULT 13
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 PERINEATICE 824 / DSM 792 / VKM B-1787;

MEDLINE=21359325; PubMed=11466286;

MeDLINE=1359325; PubMed=11466286;

MeDLINE=1359325; PubMed=11466286;

Gibson R., Ise H.M., Dubois J., Mitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).

J. Bacteriol. 183:4823-4838(2001).

PIR; C37225; C97225.

PIR; C37225; C97225.

SEQUENCE 263 AA; 29220 MW; 41D648F7237A42AB CRC64;
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 Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
 Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
Clostridium.
 ..
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 STRAIN=cv. Nipponbare;
The Rice Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution of rice
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 Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan C
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017099; AAP54000.1; -
 268 AA; 30728 MW; 58DC0E0881BEA6E1 CRC64;
 01-OCT-2001 (TrEMBLrel. 18, Created)
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Nypothetical protein CAC2643.
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Last annotation update)
263 AA.
 268 AA
 4; Mismatches
 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence)
01-OCT-2003 (TrEMBLrel. 25, Last annotat:
Putative AP2-domain DNA-binding protein.
 PRT;
PRT;
 1 SVIAKOMTYKVYMSGT 16
 Science 300:1566-1569(2003)
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3 IAKQMTYKVYMSGT 16 : | | | | | | | 94 LLKIMIYKVYADGT 107

Search completed: August 12, 2004, 06:19:35 Job time : 7.67418 secs

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1 SVIAKOMTYKVYMSGTV 17 US-09-890-463-2 83 Title: Perfect score: Sequence:

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1586107 segs, 282547505 residues Searched:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

|               |       | *              |        |     | SUMMARIES |              |           |
|---------------|-------|----------------|--------|-----|-----------|--------------|-----------|
| Result<br>No. | Score | Query<br>Match | Length | DB  | ID        | Description  |           |
| i n           | 83    | 6              | 17     | . 6 | Y97       | y97148       | Pigment p |
| 2             | 83    | 100.0          | 18     | m   | AAY97151  | Aay97151 Pig | Pigment p |
| e             | 83    | ٠.             | 25     | m   | AAY97152  |              | Pigment p |
| 4             | 83    | 100.0          | 169    | Ŋ   | ABP69949  | 6            | lour Fa   |
| ហ             | 83    |                | 169    | Ŋ   | ABP69944  | _            | Colour Fa |
| 9             | 83    | 100.0          | 200    | Ŋ   | ABP69957  |              | Colour Fa |
| 7             | 83    |                | 220    | Ŋ   | ABP69941  | _            | Colour Fa |
| 80            | 83    | 100.0          | 220    | Ŋ   | ABP69952  |              | Colour Fa |
| 6             | 83    |                | 220    | Ŋ   | ABP69925  |              | Colour Fa |
| 10            | 83    | 100.0          | 220    | S   | ABP69947  |              | Colour Fa |
| 11            | 83    | 100.0          | 220    | ഗ   | ABP69959  |              | Colour Fa |
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| 13            | 83    | 100.0          | 220    | S   | ABP69943  |              | lour Fa   |
| 14            | 83    |                | 220    | Ŋ   | ABP69955  | _            | Colour Fa |
| 15            | 83    |                | 220    | Ŋ   | ABP69929  | _            | Colour Fa |
| 16            | 83    |                | 220    | 2   | ABP69934  | _            | Colour Fa |
| 17            | 83    | 100.0          | 220    | ស   | ABP69958  | _            | Colour Fa |
| 18            | 83    | 100.0          | 220    | 5   | ABP69939  | _<br>_       | Colour Fa |
| 19            | 83    | 100.0          | 220    | S   | ABP69953  | _            | Colour Fa |
| 20            | 83    | 100.0          | 220    | 2   | ABP69938  | 80           | Colour Fa |
| 21            | 83    | 100.0          | 220    | Ŋ   | ABP69945  | 945          | Colour Fa |
| 22            | 83    | 100.0          | 220    | Ŋ   | ABP69927  | 7            | Colour Fa |
| 23            | 83    | 100.0          | 220    | Ŋ   | ABP69946  |              | Colour Fa |
| 24            | 83    |                | 220    | Ŋ   | ABP69926  | G            | lour Fa   |
| 25            | 83    | 100.0          | 220    | ເກ  | ABP69956  |              | Colour Fa |

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| 33335500000000000000000000000000000000                                                                                                 | 223<br>226<br>231<br>231<br>235                                                                            |
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## ALIGNMENTS

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The N-terminal peptides shown in AAY97147-48 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to clollow gene expression in transformed tissues) or general dyestuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters (both claimed)
 Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 N-terminal; pigment protein from coral tissue; PPCT; fluorescence;
tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet;
UV filter.
 Pigment protein from coral tissue N-terminal peptide 2.
 AAY97148 standard; peptide; 17 AA
 Claim 4; Page 42; 49pp; English.
 99AU-00008463.
 02-FEB-2000; 2000WO-AU000056.
 Dove S;
 (first entry)
 WPI; 2000-532892/48.
 (UNSY) UNIV SYDNEY
 Hoegh-Guldberg O,
 Acropora horrida.
 WO200046233-A1.
 02-FEB-1999;
 04-DEC-2000
 10-AUG-2000
 AAY97148;
RESULT 1
 AAY97148
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Sequence 17 AA;

Query Match

100.0%; Score 83; DB 3; Length 17;

Matches

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RESULT 2

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The N-terminal peptides shown in AAY97151-52 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dyestuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters (both claimed)
 Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 -terminal; pigment protein from coral tissue; PPCT; fluorescence;
.sgue marker; fluorescent marker; dyestuff; sunscreen; ultra violet;
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 70.
 Pigment protein from coral tissue N-terminal peptide 4.
 100.0%; Score 83; DB 3; L
100.0%; Pred. No. 5.6e-08;
tive 0; Mismatches 0;
 ABP69949 standard; protein; 169 AA.
 Example 2; Page 18; 49pp; English
 17
 02-FEB-2000; 2000WO-AU000056.
 99AU-00008463
 Dove S;
 1 SVIAKQMTYKVYMSGTV
 SVIAKOMTYKVYMSGTV
 Query Match
Best Local Similarity 100.
 22-JAN-2003 (first entry)
 WPI; 2000-532892/48.
 (UNSY) UNIV SYDNEY.
 Hoegh-Guldberg O,
 flower industry; e)
UV sink; sunscreen
 Porites lobata.
 WO200046233-A1.
 Sequence 25 AA;
 WO200270703-A2.
 02-FEB-1999;
 Platygyra sp.
 N-terminal;
 10-AUG-2000
 ABP69949;
 ABP69949
ID ABP6
 RESULT 4
 ò
 g
 ö
 ô
 The N-terminal peptides shown in AAY97151-52 are from pigment protein the Chom coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-600 nm and be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dyestuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters
 Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 N-terminal; pigment protein from coral tissue; PPCT; fluorescence; tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet; VV filter.
 Gaps
 Gaps
 .
0
 ..
0
 Length 18;
 Indels
 0; Indels
 Pigment protein from coral tissue N-terminal peptide 3.
100.0%; Pred. No. 3.6e-08; ive 0; Mismatches 0;
 100.0%; Score 83; DB 3; I
100.0%; Pred. No. 3.8e-08;
ive 0; Mismatches 0;
 AAY97151 standard; peptide; 18 AA.
 Example 2; Page 18; 49pp; English.
 AAY97152 standard; peptide; 25 AA.
 SVIAKQMTYKVYMSGTV 17
 1 SVIAKOMTYKVYMSGTV 17
 1 SVIAKOMTYKVYMSGTV 17
 17
 02-FEB-2000; 2000WO-AU000056
 99AU-00008463
 SVIAKOMTYKVYMSGTV
 Dove S;
 (first entry)
 17; Conservative
 Conservative
 Acropora aspera.
Montipora caliculata.
 Porites murrayensis,
 WPI; 2000-532892/48.
 (UNSY) UNIV SYDNEY
 Best Local Similarity
 Local Similarity
nes 17; Conserv
 Hoegh-Guldberg O,
 Sequence 18 AA;
 WO200046233-A1
 (both claimed)
 02-FEB-1999;
 04-DEC-2000
 10-AUG-2000
 AAY97151;
 Query Match
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Gaps

. 0

01-MAR-2002; 2002WO-GB000928.

02-MAR-2001; 2001US-0273227P.

(first entry)

04-DEC-2000

AAY97152

axaxa\*

RESULT 3

g ð

AAY97152

Matches

Best

Length 25; Indels

```
ABP69944 standard; protein; 169 AA.
 Claim 5; Page 349; 510pp; English.
 SVIAKOMTYKVYMSGTV 17
 1 SVIAKOMTYKVYMSGTV 17
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 22-JAN-2003 (first entry)
 Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
 UNIV QUEENSLAND.
 Porites murrayensis
 Karan M,
 UV sink; sunscreen
 WPI; 2002-740765/80
 (NUFA-) NUFARM LTD.
 Hoegh-Guldberg IO,
 (JONE/) JONES E L.
 Sequence 169 AA;
 WO200270703-A2.
 acid sequences
 12-SEP-2002
 white light
 Jones EL,
 ABP69944;
 UYQU
 RESULT 5
 ABP69944
 δ
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The invention relates to an isolated colour-facilitating molecule (CFM)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

non-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

cred coloured fleece. They are useful for producing coloured plant

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

uses include transducing or intensifying an image, providing additional

cred produced flavouring, beverage or juice or colouring agent. Other

uses include transducing or intensifying an image, providing additional

cred coloured flavouring, beverage or juice or colouring agent. Other

coating materials that experience UV damage e.g. plastics and car

cupholstery. CFMs are useful in the flower industry, in the development of

new varieties of flowering plants. Other contemplated uses include,

cred plastics and in fruits and vegetables to enhance their animo situations of distorted light spectra (biomatrix). The first all-protein

chromophore to be isolated was Green Fluorescent protein (GFP). The

sequences given in records ABB69924-ABP70048 represent CFM related amino
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 84
 100.0%; Score 83; DB 5; Length 169; 100.0%; Pred. No. 5.2e-07; attive 0; Mismatches 0; Indels
 Dove SG;
 Brugliera F, Mason J, Prescott M;
 ABP69957 standard; protein; 200 AA.
 Claim 5; Page 337; 510pp; English.
 SVIAKOMTYKVYMSGTV 17
 1 SVIAKQMTYKVYMSGTV 17
01-MAR-2002; 2002WO-GB000928.
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
 2001US-0329816P
 (revised)
(first entry)
 Conservative
 UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 Sest Local Similarity
 (NUFA-) NUFARM LTD.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 Sequence 169 AA;
 acid sequences
 15-OCT-2001;
 06-AUG-2003
22-JAN-2003
 white light.
 17;
 ABP69957;
 Query Match
 (UYQU)
 Matches
 RESULT 6
 ABP6995
q
 when visualised by a human eye in the absence of excitation by extraneous when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing oclouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in chromophore to be isolated was Green Pluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 .
0
 The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 .
0
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 60.
 Length 169;
 0; Indels
 Brugliera F, Mason J, Dove SG;
Prescott M;
 100.0%; Score 83; DB 5; I
100.0%; Pred. No. 5.2e-07;
 Mismatches
 0;
```

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Gaps

·;

Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen.

Montipora sp

Dove SG;

Mason J,

Brugliera F, Prescott M;

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02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928.
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 (UYQU) UNIV QUEEN (JONE/) JONES E L.
 Jones EL, Karan M
Hoegh-Guldberg IO,
 WO200270703-A2.
 Millepora sp.
 12-SEP-2002.
 white light
 ABP69952;
 RESULT 8
 ABP69952
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 g
 MX BX BX BX BX B
 The invention relates to an isolated colour-facilitating molecule (CFW)

Comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con transpenic animal which exhibits a novel colour e.g. sheep with blue or

con transpenic animal without sheep sheep or coloured plant

con franspenic animal without propic or colouring agent. Other

conses include transducing or intensifying an image, providing additional

light for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience Wy damage e.g. plastics and car

conting materials that experience to there contemplated uses include,

they warieties of flowering plants. Other contemplated uses include,

conting markers, general reporter molecules, photon traps, Wy sinks or

conting markers, general reporter molecules, photon traps, Wy sinks or

contemplate of flowering plants. Other contemplated uses include,

content of distorted light spectra (biomatrix). The first all-protein

contemplations of distorted light spectra (biomatrix). The first all-protein

contemplations of distorted light spectra (biomatrix). The first all-protein

contemplated on in records ABP69924-ABP70048 represent CRF related amino
 .
0
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule, CFM; green fluorescent protein, GFP; chromophore; blomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; OV sink; sunscreen.
 .
0
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 54
 Length 200;
 0; Indels
 Mason J, Dove SG;
 100.0%; Score 83; DB 5; L 100.0%; Pred. No. 6.3e-07;
 Mismatches
 Claim 5; Page 363-364; 510pp; English.
 Brugliera F,
 ABP69941 standard; protein; 220 AA
 Prescott M;
 ;
 1 SVIAKOMTYKVYMSGTV 17
 SVIAKOMTYKVYMSGTV 17
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 02-MAR-2001; 2001US-0273227P.
 (first entry)
 17; Conservative
 (UYQU) UNIV QUEENSLAND. (JONE/) JONES E L.
 Karan M,
 WPI; 2002-740765/80.
 Query Match
Best Local Similarity
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 (NUFA-) NUFARM LTD.
 Sequence 200 AA;
WO200270703-A2
 12-SEP-2002,
 22-JAN-2003
 white light
 ABP69941;
 Matches
 RESULT 7
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NAMES OF COLOR COL

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The invention relates to an isolated colour-facilitating molecule (CFW) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous one-white light or particle emission. CFMs are useful for producing a con-white light or particle emission. CFMs are useful for producing a coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other cast include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of coating markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental compression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs embedded in a gel matrix improve image quality in situations of distorted light species (biomatrix). The first all-protein commence of promophore to be isolated was Green Fluorescent protein (FFP). The commence of promophore to be isolated was Green Fluorescent protein (FFP). The commence of thrompolore is approved the contraction of the component protein (FFP). The commence of the component protein (FFP) is a proposed the contract of the component protein (FFP). The commence of the component protein (FFP) is a protein or the contract of the component protein (FFP). The contract of the component protein (FFP) is a protein or the contract of the contr
Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 sequences given in records ABP69924-ABP70048 represent CFM related amino
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP;
 ..
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 74.
 100.0%; Score 83; DB 5; Length 220; 100.0%; Pred. No. 7e-07; ive 0; Mismatches 0; Indels
 Claim 5; Page 330-331; 510pp; English.
 ABP69952 standard; protein; 220 AA.
 .,0
 17
 1 SVIAKOMTYKVYMSGTV
 1 SVIAKOMTYKVYMSGTV
 22-JAN-2003 (first entry)
 Query Match
Best Local Similarity 100.
 Sequence 220 AA;
 acid sequences
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extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of the varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein
 The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant
 chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 ·
0
 Score 83; DB 5; Length 220;
Pred. No. 7e-07;
Mismatches 0; Indels
 Dove SG;
 Mason J,
 Claim 5; Page 351-352; 510pp; English
 ABP69925 standard; protein; 220 AA.
 Brugliera F,
 0;
 Prescott M;
 100.0%;
100.0%;
 1 SVIAKQMTYKVYMSGTV 17
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928.
 22-JAN-2003 (first entry)
 17; Conservative
 UNIV QUEENSLAND.
JONES E L.
 Karan M,
 Local Similarity
 WPI; 2002-740765/80
 Hoegh-Guldberg IO,
 UV sink; sunscreen
 NUFARM LTD
 Sequence 220 AA;
 acid sequences
 WO200270703-A2
 Platygyra sp
 12-SEP-2002.
 white light
 Query Match
 Jones EL,
 (UYQU)
 NUFA-)
 Matches
 RESULT 9
ABP69925
 DP
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous con-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or ced coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing photorbropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or companients. CFMs modify visible colour in edible and/or cornamental colour sunscreens. CFMs modify visible colour in edible and/or cornamental colour contemblate. The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The content of the colour in records ABP69924-ABP70048 represent CFM related amino
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule; CFW; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 0;
Colour Facilitating molecule (CFM) related sequence #SEQ ID 22
 100.0%; Score 83; DB 5; Length 220; 100.0%; Pred. No. 7e-07;
 0; Indels
 Dove SG;
 Brugliera F, Mason J,
 Mismatches
 Claim 5; Page 286-287; 510pp; English.
 ABP69947 standard; protein; 220 AA.
 0;
 Prescott M;
 17
 1 SVIAKOMTYKVYMSGTV 17
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 1 SVIAKOMTYKVYMSGTV
 Local Similarity 100.
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 UV sink; sunscreen
 (JONE/) JONES E L.
 Sequence 220 AA;
 Acropora aspera.
 WO200270703-A2.
 white light.
 12-SEP-2002
 ABP69947;
 Query Match
 RESULT 10
ABP69947
ID ABP69
 Matches
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0

0

22-JAN-2003

Platygyra sp.

02-MAR-2001;

12-SEP-2002.

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RESULT 11 ABP69959

Matches

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Gaps

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17

SVIAKOMTYKVYMSGTV

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The invention relates to an isolated colour-facilitating molecule (CFW) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous con-white light or particle emission. CFMs are useful for producing a transgent animal white extinctly a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing agent. Other cases include transducing or intensifying an image, providing agent. Other cuses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car counting materials that experience UV damage e.g. plastics and car counting materials that experience UV damage e.g. plastics and car contemplated uses include. The contemplated uses include. Chevression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs mendify vishle colour in edible and/or ornamental chungal species, and in fruits and vegetables to enhance their animprove image quality in chromophore in a distorted light spectra (Diomatrix). The first all-protein chromophore in the spectra (Diomatrix). The first all-protein chromophore in the spectra (Diomatrix). The first all-protein chromophore in the colour in chromophore in the colour in chromophore in the colour in colour in chromophore in the colour in colour in colour in the colour in
 chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.)
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Colour facilitating molecule, CFM; green fluorescent protein, GFP; chromophore, biomatrix; transgenic animal, colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 88
 100.0%; Score 83; DB 5; Length 220; 100.0%; Pred. No. 7e-07; ive 0; Mismatches 0; Indels
 Brugliera F, Mason J,
 Claim 5; Page 368-369; 510pp; English.
ABP69959 standard; protein; 220 AA.
 100.08; Fr.
 Prescott M;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 17
 01-MAR-2002; 2002WO-GB000928,
 (first entry)
 SVIAKOMTYKVYMSGTV
 Query Match
Best Local Similarity 100.
Matches 17; Conservative
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 (revised)
 Karan M,
 WPI; 2002-740765/80.
 UV sink; sunscreen
 Hoegh-Guldberg IO,
 (UYQU) UNIV QUEEN
(JONE/) JONES E L.
 Sequence 220 AA;
 WO200270703-A2.
 Montipora sp.
 06-AUG-2003
 22-JAN-2003
 12-SEP-2002.
 white light.
 ABP69959;
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 Jones
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 The invention relates to an isolated colour-facilitating molecule (CFM)

Comprising a polypeptide which, in a cell, alone or together with one or

Conter molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

non-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing coloured plant

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

cation for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience U plastics and car

coating materials that experience to the flower industry, in the development of

the varieties of flowering plants. Other contemplated uses include,

coating markers, general reporter molecules, photon traps, W sinks or

in sunscreens. CFMs modify visible colour in edible and/or ornamental

companies. The species of and in a gel matrix ingrove image quality in

situations of distorted light spectra (biomatrix). The first all-protein

corression markers are useful as green Fluorescent protein (GFP). The

sequences given in records ABP69924-ABP70048 represent CFM related amino
 .;
0
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 66.
 ó
 Length 220;
 0; Indels
 Mason J, Dove SG;
 100.0%; Score 83; DB 5; 100.0%; Pred. No. 7e-07;
 Mismatches
 Claim 5; Page 344-345; 510pp; English.
 Brugliera F,
 Prescott M;
 .
 1 SVIAKOMIYKVYMSGTV 17
 SVIAKOMTYKVYMSGTV 17
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 2001US-0273227P
 01-MAR-2002; 2002WO-GB000928
 17; Conservative
 UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENS
(JONE/) JONES E L.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 sink; sunscreen
 Query Match
Best Local Similarity
 Sequence 220 AA;
 WO200270703-A2
 acid sequences
```

white light.

Dove SG;

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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or transgenic animal which exhibits a novel colour e.g. sheep with blue or extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing photortopic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, cypression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their colounity in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Pluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 52.
 Claim 5; Page 327-328; 510pp; English.
 Brugliera F,
Prescott M;
 ABP69940 standard; protein; 220 AA.
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928.
 02-MAR-2001; 2001US-0273227P.
 (first entry)
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80.
 sink; sunscreen.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 JONES E L.
 Sequence 220 AA;
 WO200270703-A2.
 Millepora sp.
 22-JAN-2003
 12-SEP-2002.
 white light
 ABP69940;
 (JONE/)
RESULT 12
 ABP69940
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Dove SG;

Mason J,

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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous conventient light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or ced coloured flace. They are useful for producing coloured plant extracts. e.g. flavouring, beverage or juice or colouring agent. Other extracts, e.g. flavouring, beverage or juice or colouring agent. Other cuses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, or markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their corramental columinate to enhance their chromophore to be isolated was Green Fluorescent protein (GFP). The chromophore to be isolated was Green Fluorescent protein (GFP). The contemporations of distorted light species thomastics and mino for sequence given in records ABP69924-ABP71048 represent CFM related amino
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 chromophore; biomatrix; transgenic animal; colouring agent;
flower industry; expression marker; reporter molecule; photon trap;
 facilitating molecule; CFM; green fluorescent protein; GFP;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 58.
 Dove SG;
 Mason J,
 ABP69943 standard; protein; 220 AA.
 Claim 5; Page 335; 510pp; English.
 Brugliera F,
 Prescott M;
17
 1 sviakomrykvymsdrv 17
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928.
 (first entry)
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Porites murrayensis.
 WPI; 2002-740765/80
 Karan M,
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 UV sink; sunscreen.
 (JONE/) JONES E L.
 WO200270703-A2
 white light
 22-JAN-2003
 12-SEP-2002
 ABP69943;
 Colour
 RESULT 13
 ABP69943
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100.0%; Score 83; DB 5; Length 220;

Sequence 220 AA;

Query Match

0

Gaps

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100.0%; Score 83; DB 5; Length 220; larity 100.0%; Pred. No. 7e-07; Conservative 0; Mismatches 0; Indels

Local Similarity es 17; Conserv

Best Loca Matches

Query Match

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Gaps

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Score 83; DB 5; Length 220; Pred. No. 7e-07; Mismatches 0; Indels

100.0%; Scc. 100.0%; Pre

Ouery Match Best Local Similarity 100. Matches 17; Conservative

Sequence 220 AA;

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17

1 SVIAKOMTYKVYMSGTV

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1 SVIAKOMTYKVYMSGTV 17

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 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
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 Indels
 Brugliera F, Mason J, Dove SG;
Prescott M;
 . 7e-07;
 Mismatches
 Pred. No.
 ABP69955 standard; protein; 220 AA.
 Claim 5; Page 359; 510pp; English.
100.08; Pre
 1 SVIAKOMTYKVYMSGTV 17
 1 SVIÁKÓMTÝKVÝMSGTV 17
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 21-MAR-2001; 2001AU-00003874.
 15-OCT-2001; 2001US-0329816P
 (first entry)
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Matches 17; Conservative
 UNIV QUEENSLAND.
 (revised)
 Karan M,
 WPI; 2002-740765/80.
 UV sink; sunscreen
 (NUFA-) NUFARM LTD.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 (UYQU) UNIV QUEENS
(JONE/) JONES E L.
 Pavona decussata
 WO200270703-A2.
 06-AUG-2003
 22-JAN-2003
 12-SEP-2002.
 white light.
 ABP69955;
 RESULT 14
 ABP69955
 g
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, and car and car are all the contemplated uses include, and car are nevertable to the contemplated uses include, and car are nevertable to the contemplated uses include, and car are nevertable to the contemplated uses include, and car are nevertable to the contemplated uses include, and car are nevertable to the contemplated uses include.
 expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924.ABP70048 represent CFM related amino acid sequences. (Updated on 06-NUG-2003 to correct OS field.)
```

```
The invention relates to an isolated colour-facilitating molecule (CFM)

Comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

non-white light or particle emission. CPMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing coloured plant

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

uses include transducing or intensifying an image, providing additional

light for growing photorbopic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

upholstery. CFMs are useful in the flower industry, in the development of

now varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs modify visible colour in edible and/or ornamental

turgal species, and in fruits and vegetables to enhance their

turgal species, and in fruits and vegetables to enhance their
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 marketability. CFMs embedded in a gel matrix improve image quality in
 Colour facilitating molecule, CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 30.
 Brugliera F, Mason J, Dove SG;
Prescott M;
 Claim 5; Page 296-297; 510pp; English.
 ABP69929 standard; protein; 220 AA.
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 02-MAR-2001; 2001US-0273227P
 (first entry)
 QUEENSLAND.
 (revised)
 Karan M,
 WPI; 2002-740765/80.
 UV sink; sunscreen
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 (NUFA-) NUFARM LTD
 (UYQU) UNIV QUEEN (JONE/) JONES E L.
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 WO200270703-A2.
 06-AUG-2003
 12-SEP-2002.
 white light.
 22-JAN-2003
 ABP69929;
RESULT 15
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situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.)
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Matches 17; Conservative 0; Mismatches 0; Indels
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(without alignments)
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 Gapop 10.0 , Gapext 0.5
 1 SVIAKOMTYKVYMSGTV 17
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-09-890-463-2
 BLOSUM62
 Scoring table:
 Perfect score:
 Database :
 Sequence:
 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| 12               | Sequence 1, Appli | 20,  | 7               | Sequence 4, Appli | Sequence 56, Appl | Sequence 32, Appl | Sequence 13, Appl | 12                 | 18   | Sequence 40, Appl | ď    | 4    | 7    | ď    | 117                    | _    | ď                 | ц,   | m                 | 76,  |      |                   | 9                     |       |       | Sequence 41, Appl   | œ               | Sequence 10, Appl | Sequence 26, Appl |
|------------------|-------------------|------|-----------------|-------------------|-------------------|-------------------|-------------------|--------------------|------|-------------------|------|------|------|------|------------------------|------|-------------------|------|-------------------|------|------|-------------------|-----------------------|-------|-------|---------------------|-----------------|-------------------|-------------------|
| US-10-081-864-12 | US-10-121-258-1   |      | US-10-315-920-2 | US-10-315-920-4   | - 1               | US-10-406-618-32  | US-10-433-640-13  | : US-10-724-178-12 | US-1 | US-10             | US-1 | US-1 | US-1 | US-1 | 3 US-10-437-963-112625 | us-  | S US-10-343-977-2 |      | 5 US-10-343-977-3 |      | ns-  | US-10-424-599-224 | 2 US-10-425-114-67457 | US-10 | US-10 | 6 US-10-423-688A-41 | US-09-976-673-8 | US-09-976-673-10  | US-09-976-673-26  |
| 14               | 14                | 14   | 14              | 14                | 15                | 15                | 16                | -                  | Н    | 14                | Н    | Ä    | 14   | Н    | Ä                      | 15   | -1                | 14   | Н                 | М    | 10   | 12                | ٦                     | 14    | Н     | Н                   | 6               | 6                 | 6                 |
| 225              | 225               | 225  | 225             | 225               | 225               | 225               | 225               | 226                | 230  | 230               | 236  | 236  | 240  | 240  | 326                    | 487  | 206               | 545  | 547               | 548  | 107  | 133               | 213                   | 215   | 222   | 225                 | 226             | 226               | 226               |
| 48.2             | 48.2              | 48.2 |                 | 48.2              | 48.2              | 48.2              | 48.2              | 48.2               | 48.2 | 48.2              | 48.2 | 48.2 | 48.2 | 48.2 | 48.2                   | 48.2 | 48.2              | 48.2 | 48.2              | 48.2 | 47.0 | 47.0              | 47.0                  | 47.0  | 47.0  | 47.0                | 47.0            | 47.0              | 47.0              |
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| 16               | 17                | - 8  | 61              | 20                | 21                | 22.               | 23                | 24                 | 25   | 26                | 27   | 28   | 29   | 30   | 31                     | 32   | 33                | 34   | . E               | 90   | 3.7  | 38                | 33                    | 40    | 41    | 42                  | 43              | 44                | 45                |

## ALIGNMENTS

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 APPLICANT: Bhattacharjee, J.
APPLICANT: Bhattacharjee, J.
APPLICANT: Bhattacharjee, Vasker
APPLICANT: Bhattacherjee, Vasker
TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
TITLE OF INVENTION: A BIOLOGICAL SAMPLE
FILE REFRENCE: 96,247-A
CURRENT APPLICATION NUMBER: US/09/994,595
CURRENT APPLICATION NUMBER: 08,650,809
PRIOR PILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Microsoft Word 97
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 ; OTHER INFORMATION: Polypeptide segment of ACVS_EMENI shown in Figure US-09-994-595-43
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 US-10-424-599-172498; Sequence 172498, Application US/10424599; Publication No. US20040031072A1
 Sequence 43, Application US/09994595
Publication No. US20030039981A1
GENERAL INFORMATION:
 1 SVIAKOMTYKVYMSGT 16
 1 SLTSKOLAYVTYTSGT 16
 ORGANISM: Artificial sequence
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US-09-994-595-43
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LENGTH: 107
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US-10-442-148A-8
 Query Match
 TYPE: PRT
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 FEATURE:
 FEATURE:
 LENGIH:
 RESULT 6
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 d
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 ò
 APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 172498
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 AFBOULT STANDARD OF A SECTION OF USZOBOLTS BORD OF A SECTION OF USZOBOLTS BORD OF A SECTION OF USZOBOLTS BORD OF A SECTION OF THE SECT
 DB 12; Length 47;
 49.4%; Score 41; DB 14; Length 225; 52.9%; Pred. No. 25; 1.ive 3; Mismatches 5; Indels
 Indels
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16 VARQPTIRIYMLGT 29
 3 IAKQMTYKVYMSGT 16
 APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
 Ouery Match
Best Local Similarity 52.3.
9; Conservative
 ORGANISM: Glycine max
GENERAL INFORMATION:
 NAME/KEY: unsure
LOCATION: (1)..(
 LENGTH: 225
 FEATURE:
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; Publication No. US20040014242A1
; GENERAL INFORMATION:
APPLICANT: IMAKURA, MASAHIRO

RESULT 4 US-10-442-148A-7

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APPLICANT: HIROTA, KIYONORI
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ORIENTATION-CONTROLLED PROTEIN AND
FILLE OF INVENTION: PROCESS FOR ARRAVING AND IMMOBILIZING PROTEIN USING THE SAME
FILLE PREERRYCE: 04583.0103-00000
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CURRENT PILING DATE: 2003-05-21
PRIOR PILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 12
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 APPLICANT: TWAKURA, MASAHIRO
APPLICANT: TWAKURA, KIYONORI
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ORIENTATION-CONTROLLED PROTEIN AND
TITLE OF INVENTION: PROCESS FOR ARRAYING AND IMMOBILIZING PROTEIN USING THE SAME
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 US-10-081-864-25

Sequence 25, Application US/10081864

Publication No. US20030022287A1

GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
APPLICANT: Saustky, Alexandr
APPLICANT: Saustky, Alexandr
APPLICANT: Savistky, Alexandr
TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-067
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 49.4%; Score 41; DB 15; Length 225; 52.9%; Pred. No. 25; cive 3; Mismatches 5; Indels
 15; Length 239;
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CURRENT FILING DATE: 2003-05-21
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PRIOR FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.2
 ; Sequence 8, Application US/10442148A; Publication No. US20040014242A1; GENERAL INFORMATION:
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6 NVITEFMRFKVRMEGTV 22
 1 SVIAKOMTYKVYMSGTV 17
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 1 SVIAKOMTYKVYMSGTV 17
 ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 Best Local Similarity 52.9
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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 RESULT 10
US-09-794-308-12
 US-09-866-538-12
 SEQ ID NO 12
 TYPE: PRT
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 ò
 g
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Sequence 46, Application US/10006922
Publication No. US20020197676A1
GENERAL INFORMATION:
APPLICANT: Ludyanov, Sergey A
APPLICANT: Labas, Yulii A.
APPLICANT: Labas, Yulii A.
APPLICANT: Labas, Yulii A.
APPLICANT: Labas, Yulii A.
APPLICANT: Matz, Mikhail V.
APPLICANT: Matz, Mikhail V.
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APPLICANT: Movention: No. US20020197676Alel Chromophores/Fluorophores and TITLE OF INVENTION: Methods for US4049, 330
PRIOR APPLICATION NUMBER: 09/458, 447
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PRIOR PLING DATE: 1999-12-09
PRIOR PLING DATE: 1999-11-19
NUMBER: OF SEQ ID NOS: 46
SEQ ID NO 46
INVENTIOR OF SEQ ID NOS: 46
INVENTIOR
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 .
 48.2%; Score 40; DB 13; Length 205; larity 52.3%; Pred. No. 34; Conservative 3; Mismatches 5; Indels
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48.2%; Score 40; DB 14; Length 26;
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Matches 9; Conservative 3; Mismatches 5; Indels
 OTHER INFORMATION: non-aggregating mutant fragment
CURRENT APPLICATION NUMBER: US/10/081,864
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: 10/006,922
PRIOR PILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
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Best Local Similarity
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 US-09-999-745-67
 US-10-006-922-46
 US-10-081-864-25
 RESULT 8
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0
 Gaps
 APPLICANT: Tsien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
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CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR ATLING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PACENTIN VERSION 3.0
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Publication No. US20030170911A1
GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, ROGER
APPLICANT: ZACHARIAS, David
APPLICANT: BAIRD, Geoffrey
TITLE OF INVENTION:
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Publication No. US2003032088A1
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APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TSIEN, Roger
APPLICANT: TSIEN, Roder
TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
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 1 SVIAKOMTYKVYMSGTV
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APPLICANT: Lukyanov, Arcady F.
APPLICANT: Lukyanov, Arcady F.
APPLICANT: Labas, Yulii A.
APPLICANT: Terakkov, Arcady F.
APPLICANT: Terskikh, Alexey
TITLE OF INVENTION: No. US20020197676Alel Chromophores/Fluorophores and
TITLE OF INVENTION: Methods for Using the Same
FILE REFERENCE: CLON-035CIP
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/457,898
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR PRIOR APPLICATION NUMBER: 09/458,144
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-11-19
 RESULT 14

US-10-006-922-44

i Sequence 44, Application US/10006922
; Publication No. US2002019767641
; GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey A
; APPLICANT: Labas, Yulii A.
APPLICANT: Labas, Yulii A.
APPLICANT: Tarakov, Arcady F.
; APPLICANT: Tarakov, Arcady F.
; APPLICANT: Matz, Mikhail V.
; APPLICANT: Matz, Mikhail V.
; APPLICANT: Tarskikh, Alexay
; TITLE OF INVENTION: Methods for Using the Same
TITLE OF INVENTION: Methods for Using the Same
; FILE REFRENCE: LOA-035CIP
; CURRENT APPLICATION NUMBER: US/10/006,922
; RIOR APPLICATION NUMBER: US/120,330
; PRIOR PILING DATE: 1999-12-09
; PRIOR FILING DATE: 1999-12-09
; PRIOR FILING DATE: 1999-12-09
; PRIOR FILING DATE: 1999-12-09
; PRIOR PILING DATE: 1999-12-09
 48.2%; Score 40; DB 13; Length 225; larity 52.9%; Pred. No. 38; Conservative 3; Mismatches 5; Indels
 NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
 RESULT 13
US-10-006-922-12
'Sequence 12, Application US/10006922
'Publication No. US20020197676A1
'GENERAL INFORMATION:
 6 NVIKEFMRFKVRMEGTV 22
 1 SVIAKOMTYKVYMSGTV 17
 6 NVIKEFMRFKVRMEGTV 22
 TYPE: PRT
ORGANISM: Discosoma species
 Query Match
Best Local Similarity
 US-10-006-922-12
 SEQ ID NO 12
 Matches
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 Sequence 12, Application US/09865291
Fublication No. US2003018622941
GENERAL INFORMATION:
APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TING, Alice
APPLICANT: ZHANG, Alice
APPLICANT: ZHANG, Alice
APPLICANT: EREBNISSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
ITILE OF INVENTION: EMESSION RATIOMETRIC INDICATORS OF PHOSPHORYLATION
CURRENT APPLICATION NUMBER: US/09/865,291
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 225
 Gaps
 Gaps
 Sequence 4, Application US/10132067

Bublication No. US20030203355A1

GENERAL INFORMATION:
APPLICANT: Bradbury, Andrew
APPLICANT: Zeytun, Almet
APPLICANT: Waldo, Geoffrey
APPLICANT: PLOOPOGOIGS: Binding Ligands With Intrinsic
TITLE OF INVENTION: Fluorobodies: Binding Ligands With Intrinsic
TITLE OF INVENTION NUMBER: US/10/132,067
CURRENT APPLICATION NUMBER: US/10/132,067

CURRENT APPLICANT: 2.21

SOFTWARE: PatentIn Ver. 2.1

LENGTH: 225
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 DB 10; Length 225; 38;
 Score 40; DB 10; Length 225;
Pred. No. 38;
 Query Match
48.2%; Score 40; DB 12; Length 225;
Best Local Similarity 52.9%; Fred. No. 38;
Matches 9; Conservative 3; Mismatches 5; Indels
 5; Indels
 5; Indels
 ; OTHER INFORMATION: red fluorescent protein (dsRED) US-10-132-067-4
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 Mismatches
 3;
 17
 6 NVIKEFMRFKVRMEGTV 22
 6 NVIKEFMRFKVRMEGTV 22
 1 SVIAKQMTYKVYMSGTV 17
 48.2%;
52.9%;
 1 SVIAKOMTYKVYMSGTV
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Best Local Similarity 52.9
Matches 9; Conservative
TYPE: PRT
ORGANISM: Discosoma sp.
 ; TYPE: PRT
; ORGANISM: Discosoma sp.
US-09-865-291-12
 TYPE: PRT
ORGANISM: Discosoma sp.
 Query Match
Best Local Similarity
Matches 9; Conserv
 US-09-794-308-12
 US-09-865-291-12
 FEATURE:
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Gaps

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Indels

APPLICATION NUMBER: 09/444,338

1 SVIAKOMTYKVYMSGTV 17

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RESULT 15

US-10-081-864-8

Sequence 8, Application US/10081864

Publication No. US20030022287A1

GENERAL INFORMATION:

APPLICANT: Lukyanov, Sergey

APPLICANT: Lukyanov, Konstantin

APPLICANT: Lukyanov, Konstantin

APPLICANT: Lukyanov, Konstantin

APPLICANT: Lukyanov, Arcady

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION:

CURRENT PELICATION NUMBER: US/10/081,864

CURRENT PELICATION NUMBER: US/06,922

PRIOR PILING DATE: 2001-02-06-19

PRIOR FILING DATE: 2001-02-21

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 8

LENGTH: 225

TYPE: PRT

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 Query Match

48.2%; Score 40; DB 14; Length 225;
Best Local Similarity 52.9%; Pred. No. 38;
Matches 9; Conservative 3; Mismatches 5; Indels
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Best Local Similarity 52.9%; Pred. No. 38;
Matches 9; Conservative 3; Mismatches 5; Indels
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 225
 ; OTHER INFORMATION: hybrid construct US-10-006-922-44
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 TYPE: PRT
ORGANISM: Artificial Seguence
FEATURE:
 q
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Search completed: August 12, 2004, 06:51:20 Job time : 35.7766 secs

1 SVIAKQMTYKVYMSGTV 17
: | | : | | | | | | |
6 NVIKEFMRFKVRMEGTV 22

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein August 12, 2004, 06:34:08; Search time 16 Seconds (without alignments) 30.060 Million cell updates/sec Run on:

US-09-890-463-1 21 1 SVIAK 5 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

206 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   | Description    |      | hypothetical prote | TO.    | phosphoprotein, bo | ribosomal protein | hypothetical prote | synaptosomal-assoc | glycogen phosphory | hypothetical prote | protamine P1 - ora | T-cell receptor be | T-cell receptor be | protamine P1 - Cer |        |        |        | ribosomal protein | hypothetical prote |        | T-cell receptor be | thyroglobulin - do | 22K superhelical D |        | T-cell receptor be |      | o. | osin light ch | g heavy chain | Ig heavy chain CRD |
|---|----------------|------|--------------------|--------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|-------------------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------------------|------|----|---------------|---------------|--------------------|
|   | ID             | L014 | I40505             | A27897 | S11127             | S17255            | 10                 | E44823             | A60521             | T14908             | I61883             | PT0551             | PT0697             | 137013             | I84439 | I39964 | 139966 | I39965            | T14910             | S55237 | PT0597             | S18401             | A61300             | PT0534 | PT0721             | 4495 | 16 | I50385        | 027           | PT0295             |
|   | DB             | 2    | N                  | ~      | ~                  | N                 | 7                  | ~                  | 7                  | (7                 | ~                  | N                  | N                  | ~                  | 7      | 7      | 7      | 7                 | Ŋ                  | 7      | 7                  | 7                  | 7                  | 7      | 7                  | ~    | ~  | ~             | ~             | 7                  |
|   | Length         | 4    | 4                  | 4      | Ŋ                  | 4                 | 4                  | 4                  | 5                  | . 2                | 4                  | 4                  | 4                  | 4                  | 4      | Ŋ      | ഗ      | ហ                 | IJ                 | Ŋ      | 5                  | 4                  | 4                  | 4      | 4                  | Ŋ    | S  | 5             | ഗ             | 5                  |
|   |                | 7.6  | 2.9                | •      | 2.9                |                   | 3.1                | 3.1                | 3.1                | 8.1                | 3.3                |                    |                    |                    |        | 3.3    |        | •                 | 3.3                | 3.3    | 3.3                | 9.8                | 9.8                | 8      | 80                 | 8    | 8  | 8.6           | 8             | 9.8                |
| ó | Query<br>Match | 4    | 4                  | 4      | 47                 | 38                |                    | 36                 | ě                  | ñ                  | 'n                 | 'n                 | 'n                 | 'n                 | m      | 'n     | m      |                   | 'n                 | m      | 'n                 | 2                  | 7                  | 7      | 7                  | 7    | N  | N             | N             | 7                  |
|   | Score          | 10   | 6                  | 6      | 6                  | 80                | 8                  | 80                 | 60                 | 80                 | 7                  | 7                  | 7                  | 7                  | 7      | 7      | 7      | 7                 | 7                  | 7      | 7                  | 9                  | 9                  | 9      | 9                  | 9    | 9  | 9             | 9             | 9                  |
|   | Result<br>No.  |      | . 71               | e      | 4                  | 2                 | 9                  | 7                  | 80                 | σι                 | 10                 | 11                 | 12                 | 13                 | 14     | 15     | 16     | 17                | 18                 | 19     | 20                 | 21                 |                    |        | 24                 | 25   | 26 | 27            | 28            | 29                 |

| seminal plasma pro 34.5K structural p 35K structural pro growth-modulating bursin - chicken hisridinol dehydro bradykinin-potenti T-cell receptor be phagocytosis-stimu phenol 2-monoxyge phospholipase C (B | hypothetical pro<br>neuropeptide Ant<br>myosin-light-cha | RESULT 1  PUD146  Carbon-monoxide dehydrogenase (EC 1.2.99.2) small chain - Pseudomonas carboxydohydrogena  C;Species: Pseudomonas carboxydohydrogena C;Species: Pseudomonas carboxydohydrogena C;Species: Pseudomonas carboxydohydrogena C;Species: Pseudomonas carboxydohydrogena C;Date: 07.5ep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993 R;Kraut, M; Hugendieck, I.; Herwig, S.; Meyer, O. R;Kraut, M; Hugendieck, I.; Herwig, S.; Meyer, O. A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotroph A;Reference number: PL0138; MUID:90055678; PMID:2818128 A;Accession: PL0146 A;Molecule type: protein C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, met C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, met C;Keywords: oxidoreductase                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| S62883<br>B44817<br>D44817<br>GKHU<br>A60898<br>A60898<br>E37196<br>F37196<br>F37196<br>A37832<br>A37832                                                                                                     | 140804<br>146627<br>1001273<br>839390<br>ALIGNMENTS      | drogenase (EC 1.2.99.2) small clas carboxydohydrogena #sequence_revision 07-Sep-1990 eck, I.; Herwig, S.; Meyer, O.; 335-341, 1989 id distribution of CO dehydrogen PL0138; MUID:90055678; PMID:281 tein the class of the consists of the class                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ииимимимиии                                                                                                                                                                                                  | 1000                                                     | (Eq. (Eq. (Eq. (Eq. (Eq. (Eq. (Eq. (Eq.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~                                                                                                                                                                       | 4 4 4 4                                                  | ase (EC<br>boxydol<br>nce_rev<br>.; Herv<br>341, 13<br>ributic<br>; MUID<br>dehyd:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 0.00.00.00.00.00.00.00.00.00.00.00.00.0                                                                                                                                                                      | ህ ነን ነን                                                  | RESULT 1 PLO146 Carbon-monoxide dehydrogenase (EC 1.2.99.2) small chain C;Species: Pseudomonas carboxydohydrogena C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #tex C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #tex C;Accasion: PL0146 A;Title: Homology and distribution of CO dehydrogenase A;Title: Homology and distribution of CO dehydrogenase A;Accession: PL0146 A;Molecule type: protein A;Molecule type: protein A;Residues: 1-4 <rra- 1-4="" <rra-="" a;residues:="" c;comment:="" carbon-monoxide="" consists="" dehydrogenase="" of="" td="" th="" th<=""></rra->                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩                                                                                                                                                                        | सं सं सं                                                 | RESULT<br>PL0146<br>Carboto<br>C;Spect<br>C;Date<br>C;Accue<br>R;Accue<br>R;Accue<br>A;Acce<br>A;Refel<br>A;Acce<br>A;Acce<br>A;Acce<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Common<br>C;Com |

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hypotherical protein 3 (4 aa) - Bacillus stearothermophilus (58pecies: Bacillus Sobrem: Bacillus (58pecies: Bacillus Bacillus Bacillus (58pecies: Bacillus Bacillu

Gaps 0 Query Match
42.9%; Score 9; DB 2; Length 4;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 3; Mismatches 0; Indels

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RESULT 3 A27897

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C;Species: Emericella nidulans, Aspergillus nidulans
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C;Accession: 730569
R;Morrice, J; MacKenzie, D.A.; Parr, A.J.; Archer, D.B.
Curr. Genet. 34, 379-385, 1998
A;Title: Isolation and characterisation of the acctyl-CoA carboxylase gene from Aspergil
A;Reference number: Z20869; MUID:99087906; PMID:9871120
 Synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
NyAlternate names: superprotein peptide 1
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Decies: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: E44823
Extlosey, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
 R.Bonamusa, L.; Baanante, I.V. Comp. Blochem. Physiol. B 95, 295-301, 1990
A.Title: Purification and characterization of glycogen phosphorylase B from skeletal mus A.Reference number: A60521; MUID:90227907; PMID:2109669
A.Accession: A60521
 0;
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 glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment) N;Alternate names: glycogen phosphorylase b C;Species: Liza ramada C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003 C;Accession: A60521
 A;Cross-references: EMBL:Y15996; NID:e1285512; PID:e1218041; PIDN:CAA75927.1
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100.0%; Pred. No. 2.8e+05;
Live 0; Mismatches 0; Indels
 Length 4;
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A;Experimental source: visual tissue
A;Note: sequence extracted from NCBI backbone (NCBIP:64247)
C;Keywords: membrane trafficking
 Pred. No. 2.8e+05;
Mismatches 0;
 DB 2; Le. 2.8e+05;
 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
A;Residues: 1-4 <MOR>
 2; Mismatches
 Score 8;
Pred. No.
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Conservative 0;
 38.1%;
25.0%;
 Query Match
Best Local Similarity 100.vv
Nora 2; Conservative
 1; Conservative
 Similarity
2; Conserv
 Query Match
Best Local Similarity
Matches 1; Conserv
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A;Status: preliminary
 2 VIAK 5
 1 IMEK 4
 1 SV 2
 N
 SV 4
 1 SV
 SV
 Best Local
Matches
 RESULT 6
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glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - Aspergillus phoenicis (fragment)
Nathernate names: glucoamylase
C;Species: Aspergillus phoenicis
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 06-Dec-1996
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 06-Dec-1996
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 06-Dec-1996
R;Acchen: 90, 1055-1067, 1981
J Biochem. 90, 1055-1067, 1981
A;Title: Purification and characterization of a minor glucoamylase from Aspergillus sait
A;Reference number: A;7897; MUID:82075730; PMID:6796572
 Tibosomal protein YmL1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae) (5.5pecies: Saccharomyces cerevisiae) (5.5pace: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-May-1997 (5.5pacesion: S1725) #Grace R. Gracesion: S1725 #sequence_revision 14-Sep-1994 #text_change 09-May-1997 FBBS Lett. 284, 51-56, 1991 #sequencing of proteins of the large ribosomal subunit from A. Reference number: S17255 #UDD:91285106; PMID:2060626 #secession: S17255 phosphoprotein, bone - chicken (fragment)
(Species: Gallus gallus (chicken)
(Species: Gallus gallus)
(Species: Gallus gallus)
(Species: Gallus)
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 A,Accession: Ā27897
A,Molecule type: protein
A,Residues: 1-4 <INO>
C,Keywords: glycosidase; hydrolase; polysaccharide degradation
 42.9%; Score 9; DB 2; Length 4; 66.7%; Pred. No. 2.88+05; ative 1; Mismatches 0; Indels
 Score 9; DB 2; Length 5;
Pred. No. 2.8e+05;
2; Mismatches 0; Indels
 Length 4;
 C; Keywords: mitochondrion; protein biosynthesis; ribosome
 DB 2;
 Score 8;
 h 42.9%;
Similarity 33.3%;
1; Conservative 2
 38.1%;
 Query Match
Best Local Similarity 66.77
Perion 2, Conservative
 A,Accession: S11128
A,Status: preliminary
A;Molecule type: protein
A,Residues: X', 2-5 <MIK2>
C,Keywords: phosphoprotein
 Query Match
Best Local Similarity
Matches 1; Conserv
 : | |
1 AVI 3
 3 VSK 5
 1 SVI 3
 3 IAK 5
 nuclear
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Query Match

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protamine Pl - Cercopithecus patas (fragment)
C;Species: Cercopithecus patas
C;Species: Cercopithecus patas
C;Dacession: 137013
R;Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A;Title: Identification of conserved potential regulatory sequences of the protamine-ence A;Reference number: 137013; MUID:94040810; PMID:8224908
 R.Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A.Reference number: PT0509; MUID:91277601; PMID:1711558
A.Recession: PT0697
 Arith: Juncional sequences of fetal T cell receptor beta chains have few N regions. A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Accession: PT0551
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 0;
 T-cell receptor beta chain V-D-J region (135-1BF) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0697
 A,Accession: 137013
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-4 <RES>
A,Residues: 1-4 <RES>
A,Cross-references: EMBL:Z12150; NID:g22814; PIDN:CAA78134.1; PID:g4377415
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 33.3%; Score 7; DB 2; Length 4; 50.0%; Pred. No. 2.8e+05; ative 1; Mismatches 0; Indels
 Score 7; DB 2; Length 4;
Pred. No. 2.8e+05;
2; Mismatches 0; Indels
 33.3%; Score 7; DB 2; Length 4; 50.0%; Pred. No. 2.8e+05; Indels
 A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-4 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
 A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-4 <FES.
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
 2; Mismatches
 protamine P1 - savannah baboon (fragment)
 33.3%;
Exp. Med. 174, 115-124, 1991
 1; Conservative
 1; Conservative
 Query Match 33.3
Best Local Similarity 50.0
Matches 1; Conservative
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
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 1 SV 2
 3 SI 4
 Matches
 RESULT 14
 RESULT 13
 RESULT 12
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 protramine P1 - orangutan (fragment)
C;Species: Pongo pygmaeus (orangutan)
C;Species: Pongo pygmaeus (orangutan)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C;Accession: 161883
R;Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A;Title: Identification of conserved potential regulatory sequences of the protamine-end A;Reference number: 137013; MUID:94040810; PMID:8224908
A;Reference number: 137013; MUID:94040810; PMID:8224908
A;Accession: 161883
A;Accession: I61883
A;Accession: 14 RBS
A;Reference number: DNA
A;Melcule type: DNA
A;Melcule type: DNA
A;Residues: 1-4 RBS
A;Cross-references: EMBL:Z12146; NID:938156; PIDN:CAA78130.1; PID:94379372
A;Molecule type: protein
A;Residues: 1-5 <BON>
C;Superfamily: glucan phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim
 hypothetical protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-8ep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T14908
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of A;Reference number: Z18261; WUID:98265918; PMID:9604882
 0
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 A;Cross-references: EMBL:Y10809; NID:g3336901; PIDN:CAA71767.1; PID:g3336902
A;Experimental source: Hamburger Schnitt
 T-cell receptor beta chain V-D-J region (126-1CG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R;Feeney, A.J.
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 Score 7; DB 2; Length 4;
Pred. No. 2.8e+05;
2; Mismatches 0; Indels
 Query Match 38.1%; Score 8; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
 0; Indels
 Query Match 38.1%; Score 8; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indel.
 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
 h 33.3%;
Similarity 33.3%;
1; Conservative ;
 Query Match
Best Local Similarity
Matches 1; Conserv
 A; Residues: 1-5 <KIR>
 3 IAK 5
 1 MAR 3
 1 SV 2
 3 SV 4
 1 SV 2
 3 SV 4
 RESULT 11
 RESULT 10
 RESULT 9
 T1490B
 I61883
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C;Species: Papio hamadryas doguera (savannah baboon)
C;Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C;Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C;Date: 10-Mar-1993
R;Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A;Title: Identification of conserved potential regulatory sequences of the protamine-enc A;Reference number: 137013; MUID:94040810; PMID:8224908
A;Reference number: 137013; MUID:94040810; PMID:8224908
A;Recession: 184439
A;Residues: preliminary; translated from GB/EWBL/DDBJ
A;Residues: 1-4 <RES>
A;Residues: 1-4 <RES>
A;Cross-references: EMBL:Z12147; NID:938134; PIDN:CAA78131.1; PID:94379349
 Query Match
33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels
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0;

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RESULT 15
139964
ribosomal protein S4 - Bacillus circulans (fragment)
C;Species: Bacillus circulans
C;Decies: Bacillus circulans
C;Decies: Bacillus circulans
C;Decies: 19-Jul-1996 #sequence\_revision 19-Jul-1996 #text\_change 19-Jul-1996
C;Accession: 139964
R;Grundy, F.J.; Henkin, T.M.
J; Bacteriol: 174, 6763-6770, 1992
A;Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A;Accession: 13964
A;Reference number: 13964
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Roctoule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: GB:M99041; NID:g143471
C;Genetics:
A;Gene: rpsD

; 0

0; Gaps

0; Indels

Query Match
33.3%; Score 7; DB 2; Length 5;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indel.

Search completed: August 12, 2004, 06:55:20 Job time : 17 secs

:|: 1 MAR 3

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3 IAK 5

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model protein search, protein ĕ

August 12, 2004, 06:21:13; Search time 13 Seconds (without alignments) 20.027 Million cell updates/sec Run on:

US-09-890-463-1 21 Title: Perfect score:

1 SVIAK 5 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

141681 segs, 52070155 residues Searched: 38 Total number of hits satisfying chosen parameters:

length: 0 length: 5 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

|           | Description      | senonobiesa 819910 | 5515 saccharomy | 0    | _          | 2 vibri    | P58705 anthopleura | P01858 homo sapien | 7          | 'n         | _          | P13973 escherichia | achat      |            | anthc      | •          | 17         | P82099 litoria rub | P41853 artioposthi | ч         | P82070 litoria rub | P82071 litoria rub |            |            | P19991 acheta dome | P54714 canis famil | m          | P38005 chlamydia t | P42562 hirudo medi | P42563 hirudo medi | P42561 hirudo medi | P58707 anthopleura | P01162 macrocallis |
|-----------|------------------|--------------------|-----------------|------|------------|------------|--------------------|--------------------|------------|------------|------------|--------------------|------------|------------|------------|------------|------------|--------------------|--------------------|-----------|--------------------|--------------------|------------|------------|--------------------|--------------------|------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| COLUMNICO | ID               | TOWN DRECH         | RM01 VEAST      | ,    | GRWM HUMAN | LUXE VIBFI | FFKA ANTEL         | TUFT HUMAN         | BIOB CITFR | BPP7 BOTIN | EI04 LITRU | TRM3 ECOLI         | ACH1 ACHFU | EOSI HUMAN | FYRI ANTEL | OCP3 OCTMI | AL14 CARMA | EI03 LITRU         | FARP ARTTR         | PSK DAUCA | RE11 LITRU         | RE21 LITRU         | RE31 LITRU | RE32_LITRU | SUGA ACHDO         | TPIS CANFA         | UC22 MAIZE | UXA4 CHLTR         | FAR3 HIRME         | FAR4 HIRME         | FLRF HIRME         | FLRN ANTEL         | FMRF MACNI         |
|           | Length DB        |                    |                 |      | 3 1        |            |                    |                    |            |            |            |                    |            |            |            |            |            |                    |                    |           | 5 1                |                    | 5 1        | 5 1        | 5 1                | 5 1                | 5 1        | 5 1                | 4                  | 4                  | 4                  | 4                  | 4                  |
| de        | Query<br>Match I | 47.6               | α               | 28.6 | ۳.         | 23.8       | 23.8               | ۳                  | ω,         | 3          | ω,         | ω.                 | 6.         | 9          | σ          | σ          | g          | 19.0               | σ                  | σ         | 19.0               | σ                  | σ          | 19.0       | g                  | 19.0               | 19.0       |                    |                    |                    |                    | 9.5                |                    |
|           | Score            | 0.5                | α               | 9 49 | . rυ       | ហ          | Ŋ                  | Ŋ                  | Ŋ          | ιΩ         | Ŋ          | ιυ                 | 4          | 4          | 4          | 4          | 4          | 4                  | 4                  | 4         | 4                  | 4                  | 4          | 4          | 4                  | 4                  | 4          | 4                  | 2                  | 2                  | 7                  | 7                  | 7                  |
|           | Result<br>No.    | -                  | 10              | m    | 4          | Ŋ          | 9                  | 7                  | σο         | 6          | 10         | 11                 | 12         | 13         | 14         | 15         | 16         | 17                 | 18                 | 19        | 20                 | 21                 | 22         | 23         | 24                 | 25                 | 26         | 27                 | 28                 | 29                 | 30                 | 31                 | 32                 |

| P01151 sus scrofa<br>P19916 pseudomonas<br>P13071 citrobacter<br>P58648 octopus min<br>P81864 pardachirus |  |
|-----------------------------------------------------------------------------------------------------------|--|
| THYL PIG<br>DCML_PSECH<br>BIOA_CITFR<br>OCPI_OCIMI<br>PAP2_PARMA                                          |  |
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| 44400                                                                                                     |  |
| 8 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                   |  |

## ALIGNMENTS

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 acceptor.
-!- COFACTOR: Binds 2 2Fe-2S clusters.
-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 MEDLINE=91285106; PubMed=2060626; Grohman L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S., Kitakawa M.;
 Gaps
 Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria.";
Arch Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.
 "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."; FEBS Lett. 284:51-56(1991).
 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycoties; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
 -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
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 Pseudomonas carboxydohydrogena.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae.
 PIR; PL0146; PL0146.
Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.
NON TER
SEQÜENCE 4 AA; 420 MW; 6DD33DD6F000000 CRC64;
 Similarity 66.7%; Pred. No. 1.48+05;
2; Conservative 1; Mismatches 0; Indels
 (Fragment)
 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase small chain (EC 1.2.99.2)
dehydrogenase subunit S) (CO-DH S) (Fragment).
 P36515;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Mitochondrial 60S ribosomal protein L1 (YmL1)
MRPL1.
 4 AA.
 4 AA
 PRT;
 PRT;
 SEQUENCE.
MEDLINE=90055678; PubMed=2818128;
 STANDARD;
 STANDARD;
 Query Match
Best Local Similarity
Matches 2; Conserv
 :||
1 MAK 3
 NCBI_TaxID=290;
 3 IAK 5
 RM01 YEAST
 PSECH
 SEQUENCE
 P19918;
RESULT 1
DCMS_PSECH
 RESULT 2
RM01_YEAST
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Best Local Similarity
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 RESULT 5
LUXE_VIBFI
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 RESULT 6
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 EXPUENCE.
MEDLINE=77162369; PubMed=858356;
MEDLINE=77162369; PubMed=858356;
Schlesinger D.H., Pickart L., Thaler M.M.;
Schlesinger D.H., Pickart L., Thaler M.M.;
"Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
Experientia 33:324-325.[1977).
-!- MISCELLANEOUS: This serum tripeptide has been found to stimulate growth of some cell types and to inhibit other types in vitro.
GO: GO:0001558; P:regulation of cell growth, NAS.
SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;
 Gaps
 0; Gaps
 Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K., Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis."; Electrophoresis 15:735-745(1994).

-!- MISCELLANBCUS: On the 2D-gel the determined pI of this unknown protein is: 6.6, its MW is: 19 kDa.
 01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annocation update)
Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 0:
 1; Indels
 0; Indels
 Query Match
38.1%; Score 8; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indele
 Score 6; DB 1; Length 5; Pred. No. 1.4e+05; 1; Mismatches 1; Indel:
 NON TER 4 4 SEQUENCE 4 AA; 402 MW; 7771B2D5D000000 CRC64;
 SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;
 21-JUL_1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
20-VUL-modulating peptide.
Homo sapiens (Human).
 3 AA.
 5 A.A.
 PRT;
 PRT;
PIR, S17255, S17255.
SGD; L0002681; MRPL1.
Ribosomal protein; Mitochondrion.
 SEQUENCE.
TISSUB-Fibroblast;
MEDLINE-95009907; PubMed=7523108;
 h 28.6%;
Similarity 33.3%;
1; Conservative
 STANDARD;
 STANDARD;
 Query Match
Best Local Similarity
Matches 1; Conserv
 3 IAK 5
 IGR 4
 1 SV 2
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 GRWM HUMAN
 UF01 MOUSE
 RESULT 3
UF01 MOUSE
 RESULT 4
GRWM HUMAN
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Query Match

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 01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
 MEDLINE-9107226; PubMed=2254256;
MEDLINE-9107226; PubMed=2254256;
Swatzman E., Kapoor S., Graham A.F., Meighen E.A.;
Swatzman E., Kapoor S., Graham A.F., Meighen E.A.;
"A new Vibrio fischeri lux gene precedes a bidirectional termination site for the lux operon.";
J. Bacteriol. 172:6797-6802 (1990).
-!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING THE LUCIFERASE-CATALXZED REACTION.
SUBSTRATE IN THE LUCIFERASE-CATALXZED REACTION.
-!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thiolester.
-!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 Gaps
 Gaps
 Anthopleura elegantissima (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
 ·.
 .,
 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio. VCBI_TaxID=668;
 Indels
 0; Indels
 DB 1; Length 3; . 1.4e+05;
 1 1 1
3 AA; 374 MW; 6AA330300000000 CRC64;
100.0%; Pred. No. 1.4e+05; ive 0; Mismatches 0;
 Last sequence update)
Last annotation update)
 Ą.
 4 AA.
 23.8%; Score 5; DB 1 100.0%; Pred. No. 1.4 ative 0; Mismatches
 EMBL; M62812; -; NOT_ANNOTATED_CDS.
Luminescence; Ligase.
 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last seq. 28-FEB-2003 (Rel. 41, Last anno
 01-MAR-1992 (Rel. 21, Created)
 protein synthetase) (Fragment)
 1; Conservative
 STANDARD;
 1; Conservative
 STANDARD;
 Local Similarity
 Vibrio fischeri.
 Antho-Khamide.
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 01-MAR-1992
01-OCT-1996
 7.
 FFKA ANTEL P58705;
 SECUENCE
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 cell membrane of neutrophils in the blood. Leucokininase on the membrane releases the active peptide tuftsin from the gamma chain. Tuftsin is essential for maximum stimulation of the phagocytic
 .nemistry 6:3386-3392(1967).
MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the
 Gaps
 Grimmelikhuijzen C.J.P.;
 MEDLINE=68091045; PubMed=4169272; Fidalgo B.V., Najjar V.A.; Fidalgo B.V., Najjar V.A.; "The physiological role of the lymphoid system. VI. The stimulatory effect of leucophilic gamma globulin (leucokinin) on the phagocytic activity of human polymorphonuclear leucocyte."; Blochemistry 6:3386-3392(1967)
 MEDLINE=93391436; PubMed=8397415; MEDLINE=93391436; PubMed=8397415; McFarlane I.D., Nochacker H.-P., Grimmelikhuijzen C.J.P. "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-Khamide and Antho-Rhamide."; Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
 MEDLINE=72187087; PubMed=4112769; Mishioka K., Constantopoulos A., Satch P.S., Najjar V.A.; Nishioka K., Constantopoulos A., Satch P.S., Najjar V.A.; The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin."; Biochem. Biophys. Res. Commun. 47:172-179(1972).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.; "Isolation of L-3-phenyllactyl-bhe-lys-Ala-NH2 (Antho-KAamide), novel neuropeptide from sea anemones."; Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
 .
 0; Indels
 DB 1; Length 4;
 23.8%; Score 5; DB 1; Length 4; 100.0%; Pred. No. 1.4e+05; ive 0; Mismatches 0; Indels
 GO:0006909; P:phagocytosis; NAS.
UENCE 4 AA; 501 MW; 74176321C000000 CRC64;
 4 4 AA; 512 MW; 6DD339C9A000000 CRC64;
 23.8%; Score 5; DB 1; Le 100.0%; Pred. No. 1.4e+05; iive 0; Mismatches 0;
 L-3-PHENYLLACTYL.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
 4 AA.
 Phagocytosis-stimulating peptide (Tuftsin)
 -!- SUBCELLULAR LOCATION: Secreted.
 GO; GO:0003823; F:antigen binding; NAS.
 PRT;
MEDLINE=92028852; PubMed=1681803;
 activity of neutrophils.
 Neuropeptide; Amidation.
 1; Conservative
 STANDARD;
 IMMUNOGLOBULIN CLASS.
 Query Match
Best Local Similarity
 Homo sapiens (Human)
 PIR; A02147; A02147.
MIM; 191150; -.
 PIR; JQ1273; JQ1273
 Query Match
Best Local Similarity
 NCBI_TaxID=9606;
 S
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 -14
 TUFT HUMAN
 MOD_RES
MOD_RES
SEQUENCE
 SEQUENCE
 SEQUENCE
 FUNCTION
 P01858;
 TUFT_HUMAN
 Best Loc
Matches
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 MEDLINE=89006280; PubMed=2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
citrobacter freundii and Salmonella typhimurium biotin operons.";
 Gaps
 01-APR-1993 (Rel. 25, Created)
1-FBB-1994 (Rel. 28, Last sequence update)
28-FBB-2003 (Rel. 41, Last amoctation update)
Bradykinin-potentiating peptide S5,2 (SA) (Angiotensin-converting
 Eukaryota, Metazoa, Chordata, Craniata, Verrebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Viperidae, Crotalinae, Bothrops.
 -! - CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
-! - PATHWAY: Biotin biosynthesis; last step.
-! - SIMILARITY: Belongs to the biotin and lipoic acid synthetases
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
 .,
 01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment)
 0; Indels
 Bothrops insularis (Island jararaca) (Queimada jararaca)
 Length 5;
 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;
 23.8%; Score 5; DB 1; Le 50.0%; Pred. No. 1.4e+05; tive 1; Mismatches 0
 EMBL; M21922; -; NOT_ANNOTATED_CDS.
PIR; 140698; 140698.
Biotin biosynthesis; Iron-sulfur; Transferase.
 5 A.A.
 IISSUE=Venom;
MEDLINE=90351557; PubMed=2386615;
Cintra A.C.O., Vieira C.A., Giglio J.R.;
 01-JAN-1990 (Rel. 13, Created)
 Conservative
 STANDARD;
 STANDARD;
 Gene 67:203-211(1988).
 Citrobacter freundii
 Local Similarity
 SEQUENCE FROM N.A.
 enzvme inhibitor)
 NCBI_TaxID=546;
 3 IA 4
:-|
1 MA 2
 BPP7 BOTIN
P30425;
 CITFR
 family
 SEQUENCE
 SECUENCE
 Query Match
 NON TER
 P12997
 BPP7_BOTIN
 Best Loc
Matches
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 RESULT 9
RESULT 8
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Indels

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structure and biological activity of bradykinin potentiating
 Gaps
 Gaps
 TISSUE=Skin secretion, Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; Webtides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria rubella.";
 Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae;
 Plasmid IncFII R100.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 ;0
 ..
 peptides from Bothrops insularis snake verom.";
J. Protein Chem. 9:221-227(1990).
-1- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.

PIR, G37196, G37196.
Hypotensive agent; Pyrrolidone carboxylic acid.
MOD RES
1 PYROLIDONE CARBOXYLIC ACID.
SEQÜENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;
 0; Indels
 0; Indels
 DB 1; Length 5; 1.4e+05;
 23.8%; Score 5; DB 1; Length 5; 50.0%; Pred. No. 1.4e+05;
 5 5 AMIDATION.
5 AA; 616 MW; 61F2D1A059A00000 CRC64;
 28 FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 5 AA.
 5 A.A.
 23.8%; Score 5; DB 1
100.0%; Pred. No. 1.4
live 0; Mismatches
 1; Mismatches
 Amphibian defense peptide; Amidation
 Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
 Enterobacteriaceae; Escherichia
 1; Conservative
 Local Similarity 50.0
nes 1; Conservative
 STANDARD;
 STANDARD;
 Pelodryadinae, Litoria.
NCBI_TaxID=104895;
 Tram protein (Fragment)
 Query Match
Best Local Similarity
Matches 1; Conserv
 SEQUENCE FROM N.A.
 Escherichia coli
 NCBI_TaxID=562;
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 28-FEB-2003
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 TRM3 ECOLI
 SEQUENCE
 RESULT 10
E104 LITER
AC P82107;
DT 28-FEB-20
DT 28-FEB-20
DT 10-OCT-20
DE E1ectrin
OC Bitaryota OC Butaryota OC Butaryota OC Pelodryac
OC NOBL Taxx
RN [1] Laxx
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 SEQUENCE
 Query Match
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Matches
 RESULT 11
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 ö
 Achatin-I.
Achatina fulica (Giant African snail).
Elwaryota, Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidee; Achatina.
 Gaps
 Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K., Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P., Novales B.T., Kanapi C.G., Takeuchi H., Nomoto K., Andratin-I, an endogenous neuroexcitatory terrapepiide from Achatina fulica Ferussac containing a D-amino acid residue.",
 Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K., Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
"Purification of achatin-1 from the atria of the African giant snail, Achatina fulica, and its possible function.";
Biochem. Biophys. Res. Commun. 177:847-853(1991).
 and tray genes of plasmid R100.";
J. Bacteriol. 170:2749-2757(1988)
-!- FUNCTION: TRANSFR GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the tram family.
Inamoto S., Yoshioka Y., Ohtsubo E.;
"Identification and characterization of the products from the traJ
 MEDLINE=93014529; PubMed=1399265; Biblida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Momoto K., "Crystal structure and molecular conformation of achatin-I (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid residue."; D-ept. Protein Res. 39:258-264(1992).
 0;
 0; Indels
 Length 5;
 Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;
 23.8%; Score 5; DB 1; Le. 100.0%; Pred. No. 1.4e+05; ive. 0; Mismatches 0;
 Last sequence update)
Last annotation update)
 4 AA.
 SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 STRAIN-Ferussac; TISSUE-Heart atrium;
MEDLINE-91264856; PubMed=1675568;
 EMBL; M20941; -; NOT_ANNOTATED_CDS.
 PRT;
 PIR; A32014; A32014. Conjugation; Plasmid; DNA-binding.
 STRAIN=Ferussac; TISSUE=Ganglion; MEDLINE=89273551; PubMed=2597281;
 (Rel. 29, Created)
(Rel. 29, Last seq
(Rel. 36, Last and
 1; Conservative
 STANDARD;
 X-RAY CRYSTALLOGRAPHY
 Query Match
Best Local Similarity
 NCBI_TaxID=6530;
 CHARACTERIZATION
 Ŋ
 01-JUN-1994
01-JUN-1994
 15-JUL-1998
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Query Match
Best Local Similarity
Matches 1; Conserv
 Query Match
Best Local Similarity
 TISSUE=Brain;
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P58649;
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SEQUENCE
 SEQUENCE
 MOD_RES
MOD_RES
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 Matches
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 Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

-!- MISCELLANEOUS: These peptides are released from mast cells in lung (and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt.

GO; GO:0006935; P:immune response; IDA.

V -> A (IN OTHER PEPTIDE).
-!- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency and produces a spike broadening of the identified heart excitatory neuron (PON); also enhances the amplitude and frequency of the heart beat. Has also an effect on several other muscles.

PIR; A32480; A32480.

Hormone; D-amino acid.
 "Purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of
 Gaps
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Anthopleura elegantissima (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
 .;
0
 0;
 0; Indels
 0; Indels
 19.0%; Score 4; DB 1; Length 4; 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0; Indelt
 DB 1; Length 4; . 1.4e+05;
 1 1 / Y -> A (IN OTHER PEPTIDE).
4 AA; 390 MW; 6B05B862A0000000 CRC64;
 4 AA; 408 MW; 6AADD9C81000000 CRC64;
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Antho-RIamide I (Contains: Antho-Riamide II).
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
Eosinophilotactic peptides.
 D-PHENYLALANINE.
 4 AA.
 4 AA.
 0; Mismatches
 Score 4; I
Pred. No.
 SEQUENCE.
MFDLINE=76078412; PubMed=1060093;
 MEDLINE=92270459; PubMed=1821096;
 19.0%;
 Goetzl E.J., Austen K.F.;
 1; Conservative
 STANDARD;
 Conservative
 STANDARD;
 Homo sapiens (Human)
 Query Match
Best Local Similarity
Matches 1; Conserv
 Local Similarity
 NCBI_TaxID=6110;
 anaphylaxis."
 2 V 2
 RESULT 14
FYRI ANTEL
ID FYRI ANTEL
AC PS8706;
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A
 EOSI HUMAN
ID EOSI HUMAN
AC P02731;
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 SEQUENCE
 SEQUENCE
 SEQUENCE
 Query Match
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Matches
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0
 0;
 Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D., Grimmelikhuijzen C.J.P.,
Grimmelikhuijzen C.J.P.,
"Isolation of two novel neuropeptides from sea anemones: the unusual, biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its des-phenyllactyl fragment Tyr-Arg-Ile-NH2.";
Peptides 12:1165-1173(1991).
 MCFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.,
"The expansion behaviour of sea anemones may be coordinated by two
inhibitory neuropeptides, Antho-Khamide and Antho-Rlamide.";
Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188(1993).
Proc. R. Soc. Lond., B. Biol. Sci. 253:183-188(1993).
Proc. R. Soc. Inhibits spontaneous contractions in several muscle
groups. May be involved in the expansion phase of feeding
Dehaviour in sea anemones.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Neuron specific.
Neuropeptide; Amidation.
 Gaps
 Gaps
 Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
NCBL_TaxID=89766;
 ..
 .,
 SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
 19.0%; Score 4; DB 1; Length 4; 100.0%; Pred. No. 1.4e+05; ive 0; Mismatches 0; Indels
 19.0%; Score 4; DB 1; Length 4; 100.0%; Pred. No. 1.4e+05; ive 0; Mismatches 0; Indels
 2 D-SERINE (IN OCP-4).
4 AA, 463 MW; 6AB365B810000000 CRC64;
 4 AA; 598 MW; 60441B59A000000 CRC64;
 ANTHO-RIAMIDE I.
ANTHO-RIAMIDE II.
L-3-PHENYLLACTYL.
AMIDATION.
 -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
-!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
 28-FEB-2003 (Rel. 41, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cardioactive peptides Ocp-3/Ocp-4.
 4 AA.
 active than Ocp-3.
 PRT;
 FUNCTION.
MEDLINE=93391436; PubMed=8397415;
 19.0%;
 1; Conservative
 Conservative
 STANDARD;
 Hormone; D-amino acid.
```

Search completed: August 12, 2004, 06:53:27 Job time : 14 secs

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Rattus sp.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10118;
 Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
"ILME: a waterborne pheromonal peptide released by the eggs of Sepia
 Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
 MEDLINE=91282758; PubMed=1840486; Sato H., Aono S., Kashiwamata S., Koiwai O.; Sato H., Aono S., Kashiwamata S., Koiwai O.; "Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn tat."; 17:1161-1164 (1991). EMBL; S38636; AAB19259.1;
 SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
 33.3%; Score 7; DB 11; Length 4; ilarity 33.3%; Pred. No. 1e+06; Conservative 2; Mismatches 0; Indels
 Score 5; DB 5; Length 4;
Pred. No. 1e+06;
2; Mismatches 0; Indel.
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Bilirubin UDP-glucuronosyltransferase (Fragment).
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 NON TER 1 1 SEQUENCE 4 AA; 473 MW; 633732C42000000 CRC64;
 4 AA; 505 MW; 6B1697203000000 CRC64;
 officinalis.";
Biochem. Biophys. Res. Commun. 275:217-222 (2000)
 4 AA.
 GO; GO:0016740; F:transferase activity; IEA
 Pheromone peptide ILME.
Sepia officinalis (Common cuttlefish).
 PRT;
 23.8%;
ilarity 0.0%; I
Conservative
 PRELIMINARY;
 Similarity
1; Conserva
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 TIŠSUE=Egg;
PubMed=12207899;
 TISSUE=Egg;
PubMed=10944467;
 NCBI_TaxID=6610;
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 SPECTROMETRY.
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 STRAIN-Gunn;
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 SEQUENCE
 Query Match
Best Local (
 SEQUENCE
 P83568;
 P83568
 Matches
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 RESULT 2
 P83568
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 Q08433 rattus sp.
P83568 sepia offic
P83073 bacillus ce
Q9907 hordeum vul
P83308 gallus gall
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 (without alignments)
21.035 Million cell updates/sec
 Description
 August 12, 2004, 06:32:33 ; Search time 75 Seconds
 9
 Compugen Ltd
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
 Total number of hits satisfying chosen parameters:
 4 AA.
 1017041 segs, 315518202 residues
 ALIGNMENTS
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 099007
P83308
P83570
 Q08433;
01-NOV-1996 (TrEMBLrel. 01, Created)
 Q08433
P83568
 SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_bungi:*
4: sp_human:*
5: sp_invertebrate:*
5: sp_mammal:*
5: sp_mc:*
5: sp_mc:*
5: sp_mc:*
5: sp_mc:*
5: sp_mc:*
5: sp_mc:*
 sp_rodent:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
 P83073
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 П
 sp_rvirus:*
sp_bacteriap:*
 sp archeap:*
 111
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110
113
 Query
Match Length DB
 sp_plant:*
 US-09-890-463-1
 PRELIMINARY;
 1 SVIAK 5
 length: 0
length: 5
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Gaps

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Minimum DB seq Maximum DB seq

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score:

Title:

Sequence: Perfect

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Scoring table:

Searched:

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RESULT 1 Q08433 ID Q084: AC Q0844 DT 01-N

Score

Result No.

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NCBI_TaxID=9031;
 TISSUE=Brain;
PubMed=6137771;
 PubMed=9437704;
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 FAMILY
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 Query Match
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 P83570
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 Gaps
 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Hordeum.
NCBI_TaxID=4513;
 Gaps
 MEDLINE=91329704; PubMed=1831055;
MEDLINE=91329704; PubMed=1831055;
Jacobsen J.V., Close T.J.;
"Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature bareley aleurone layers.";
plant Mol. Biol. 16:713-721(1991).
EMBL; X54643; CAA38455.1;
 .,
 ·.
 0; Indels
 88 kDa protein (Fragment).
Bacillus cereus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1396;
 DB 10; Length 5; 1e+06;
 0; Indels
 Length 5;
 P83073;
01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Created)
Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 5 AA; 623 MW; 6B01AAA336F00000 CRC64;
 5 AA; 600 MW; 61E3344DD6F00000 CRC64;
 23.8%; Score 5; DB 2; I
100.0%; Pred. No. 1e+06;
cive 0; Mismatches 0
 5 AA.
 5 A.
 23.8%; Score 5; DB 1
50.0%; Pred. No. 1e+0
iive 1; Mismatches
 Created)
 STRAIN=NCIMB 11796,
Browne N., Dowds B.C.A.,
Submitted (JUL-2001) to Swiss-Prot.
 P83308;
01-JUN-2002 (TEBMBLrel. 21,
01-JUN-2002 (TEBMBLrel. 21,
01-JUN-2003 (TEBMBLrel. 24,
 (TrEMBLrel. 01,
 -NOV-1996 (TrEMBLrel. 01, -MAR-2003 (TrEMBLrel. 23,
 Best Local Similarity 100.
Matches 1; Conservative
 AMY1 GENE.
Hordeum vulgare (Barley).
 Alpha amylase (Fragment).
 1; Conservative
 PRELIMINARY;
 PRELIMINARY;
 PRELIMINARY;
 Query Match
Best Local Similarity
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 01-NOV-1996
01-NOV-1996
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 Query Match
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 Matches
 RESULT 5
P83308
ID P8330
AC P8330
DT 01-J1
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 FMRFamide-like neuropeptide (LPLRF-amide).
Gallus gallus (Chicken).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.; "A novel active pentapeptide from chicken brain identified by antibodies to FMREmide.";
Nature 306:328-330(1983)
-!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 Gaps
 Gaps
 Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
COLI_TaxID=6610;
 ·,
 .
 Score 2; DB 13; Length 5; Pred. No. 1e+06; 0; Indels 1; Mismatches
 1; Indels
 Score 0; DB 5; Length 2;
Pred. No. 1e+06;
0; Mismatches 1; Indels
 GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
Neuropeptide; Amidation.
MOD_RES 5 AMIDATION.
 SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION TISSUE-Optic lobe;
 01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Neuropeptide GWa.
Sepia officinalis (Common cuttlefish).
 5 AA; 645 MW; 69D4073767400000 CRC64;
 MOD_RES 2 AMIDATION.
SEQUENCE 2 AA; 261 MW; 73781000000000 CRC64;
 2 AA
 Search completed: August 12, 2004, 06:54:52
Job time : 75 secs
 0.0%;
0.0%; I
 9.5%;
 0.0%;
 Local Similarity 0.04
les 0; Conservative
 PRELIMINARY;
 0; Conservative
 SEQUENCE, AND SYNTHESIS.
 Query Match
Best Local Similarity
Matches 0; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

using sw model - protein search, OM protein

August 12, 2004, 06:20:13; Search time 90 Seconds (without alignments) 15.697 Million cell updates/sec Run on:

US-09-890-463-1 21 score:

1 SVIAK 5 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Searched:

length: length: Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2003s:\*
geneseqp2003as:\*
geneseqp2003bs:\* A\_Geneseq\_29Jan04:\* geneseqp1980s:\* geneseqp1990s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|        |       | •          |              |    | SUMMARIES |             |           |
|--------|-------|------------|--------------|----|-----------|-------------|-----------|
| Result |       | *<br>Query |              |    |           |             |           |
| No.    | Score | Match      | Match Length | 80 | DI        | Description | no        |
| п      | 2     | 0          |              | m  | AY9       | y97147      | Pigment p |
| 73     | 21    | 100.0      | 5            | Ŋ  | ABB99061  | Abb99061 1  | N-termina |
| c      | 16    | 76.2       | 5            | 7  | AAR72928  |             | Yeast PPI |
| 4      | 16    | 76.2       | 5            | 7  | AAR72927  | Aar72927    | Yeast PPI |
| 5      | 16    | 76.2       | 5            | 7  | AAR72884  | Aar72884    | Yeast PPI |
| 9      | 16    | 76.2       | 5            | 9  | AA029981  | Aa029981    | Peptide # |
| 7      | 16    | 76.2       | Ŋ            | 7  | ABR63446  | Abr63446 ]  | Rat purin |
| 80     | 15    | 71.4       | 5            | Н  | AAP97806  | Aap97806    | Sequence  |
| 9      | 14    | 66.7       | 4            | 7  | AAR61324  |             | Fragment  |
| 10     | 14    | 66.7       | 5            | Ŋ  | AAY07986  |             | Human sec |
| 11     | 13    | 61.9       | 4            | Н  | AAP91629  |             | Motif use |
| 12     | 13    | 61.9       | 4            | Н  | AAP97808  |             | Sequence  |
| 13     | 1.3   | 61.9       | 4,           | 7  | AAW55770  |             | Immunisat |
| 14     | 13    | 61.9       | 4            | Ŋ  | ABB84333  | Abb84333    | Human MBP |
| 1.5    | 13    | 61.9       | 4            | 7  | ABR57300  | Abr57300    | Thermus o |
| 16     | 13    | 61.9       | ഗ            | 7  | AAR12661  | Aar12661    | Pentapept |
| 17     | 13    | 61.9       | S            | ~  | AAR51525  | Aar51525    | Mimotope  |
| 18     | 13    | 61.9       | 5            | 7  | AAR69893  | Aar69893    | Pentameri |
| 19     | 13    | 61.9       | S            | 7  | AAR78989  | Aar78989    | p107 pept |
| 20     | 13    | 61.9       | S            | 7  | AAR98639  | Aar98639    | Peptide 1 |
| 21     | 12    | 57.1       | 4            | 7  | AAR15757  | . Aar15757  | Farnesyl- |
| 22     | 12    | 57.1       | 4            | ~1 | AAR49753  | Aar49753    | Farnesylt |
| 23     | 12    | 57.1       | 4            | 7  | AAR77816  | Aar77816    | Farnesyl  |
| 24     | 12    | 57.1       | 4            | 7  | AAW04443  |             | Farnesyl  |
| 25     | 12    | 57.1       | 4            | N  | AAW65412  | Aaw65412    | Peptide u |

| Aay28344 Peptide f<br>Aay87947 Mammalian<br>Aag65468 Substrate |                                        | Abj05144 T-cell su<br>Abp63437 Monocyte<br>Aae20561 Soybean d | Abu79151 Prenylati<br>Adc26827 Anti-angi<br>Add11758 T cell su |                                  |                                  | Aar66898 Agonist p |
|----------------------------------------------------------------|----------------------------------------|---------------------------------------------------------------|----------------------------------------------------------------|----------------------------------|----------------------------------|--------------------|
| AAY28344<br>AAY87947<br>AAG65468                               | AAB57922<br>AAB55665<br>AAB80566       | ABJ05144<br>ABP63437<br>AAE20561                              | ABU79151<br>ADC26827<br>ADD11758                               | AAP61368<br>AAR11930<br>AAR51510 | AAR71699<br>AAR71698<br>AAR69878 | AAR66898           |
| 01 00 00 00<br>01 00 00 00                                     | * 4 4 4                                | 44 44<br>N N N                                                | 9 7 7                                                          |                                  | 200                              | 2                  |
| 57.1                                                           | 57.1<br>57.1<br>57.1                   | 57.1<br>57.1<br>57.1                                          | 57.1<br>57.1<br>57.1                                           | 57.1<br>57.1<br>57.1             | 57.1<br>57.1<br>57.1             | 57.1               |
| 177                                                            | 7777                                   | 122                                                           | 1222                                                           | 1222                             | 122                              | 12                 |
| 22<br>27<br>28<br>28                                           | 33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                         | 33.00                                                          | ) & 4 4<br>0 0 1                 | 44 44<br>52 52 44                | 45                 |

## ALIGNMENTS

N-terminal; pigment protein from coral tissue; PPCT; fluorescence; tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet; UV filter. Pigment protein from coral tissue N-terminal peptide 1. AAY97147 standard; peptide; 5 AA. (first entry) 04-DEC-2000 AAY97147; RESULT 1 AAY97147 

Acropora aspera.
Acropora horrida.
Montipora caliculata.
Montipora monasteriata. Porites murrayensis. Porites lobata.

WO200046233-A1.

10-AUG-2000.

02-FEB-2000; 2000WO-AU000056. 99AU-00008463 02-FEB-1999;

Dove S; (UNSY ) UNIV SYDNEY. Hoegh-Guldberg O,

Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff. WPI; 2000-532892/48.

Claim 3; Page 42; 49pp; English.

The N-terminal peptides shown in AAY97147-48 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dysetuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters

all-protein

N

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SVIAK 5
 SVIAK 5
 2 VIAK 5
 Sequence 5 AA;
 Sequence 5 AA;
 (TOFU) TONEN
 19-JUL-1990;
 19-JUL-1990;
 19-JUL-1989;
 16-OCT-2003
 29-NOV-1995
 EP647714-A1
 12-APR-1995
 06-OCT-1989
 29-DEC-1989
 AAR72928;
 proteins
 Matches
 RESULT 3
 82888
 ò
 셤
 à
 The invention relates to an isolated colour-facilitating molecule (CFM)

Comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

coloured fleece. They are useful for producing coloured plant

coloured fleece. They are useful for producing agent. Other

cuses include transducing or intensifying an image, providing additional

light for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

upholstery. CFMs are useful in the flower industry, in the development of

new varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs modify visible colour in edible and/or ornamental

C fungal species, and in fruits and vegetables to enhance their

marketability. CFMs embedded in a gel matrix improve image quality in
 ;
0
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 industry; expression marker; reporter molecule; photon trap;
 Colour facilitating molecule, CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent;
 0;
 Score 21; DB 3; Length 5;
Pred. No. 1.4e+06;
 0; Indels
 Dove SG;
 Mason J,
 0; Mismatches
 N-terminal amino acid sequence of a CFM #1.
 Brugliera F,
Prescott M;
 Claim 3; Page 278; 510pp; English.
 ABB99061 standard; peptide; 5 AA.
 100.0%;
 2001US-0273227P.
2001AU-00003874.
 01-MAR-2002; 2002WO-GB000928
 15-OCT-2001; 2001US-0329816P
 (first entry)
 5; Conservative
 QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 Local Similarity
 flower industry; ev
UV sink; sunscreen
 Hoegh-Guldberg IO,
 (NUFA-) NUFARM LTD
 JONES E L.
 1 SVIAK 5
 Ŋ
 SVIAK
 WO200270703-A2
 Sequence 5 AA;
(both claimed)
 Unidentified.
 02-MAR-2001;
21-MAR-2001;
 22-JAN-2003
 12-SEP-2002.
 white light.
 ABB99061;
 Jones EL,
 Query Match
 (UYQU)
 Matches
 RESULT 2
 ABB99061
SXS
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0
 -2003 to
(Updated
 AAR72921-29 are tryptic fragments of a yeast PPIase (peptidy) prolyl cis trans isomerase). The yeast PPIase has a single mol. wt. of about 17 kba and a single isoelectric point of about 6.2. The enzyme catalyses the isomerisation of prolyl peptide bonds in proteins and accelerates the folding of the protein. The inventors are claiming a PPIase-beta. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003) to correct PF field.) (Updated on 25-MAR-2003) to correct PR field.)
 New B.coli peptidyl prolyl cis trans isomerase beta - used to accelerate the folding of proteins, partic. for activation of inactive recombinant
 Gaps
 Gaps
situations of distorted light spectra (biomatrix). The first all-prochromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a colour-facilitating molecule (CFM)
 Escherichia coli, protein conformation, folding, acceleration, PPIase-alpha, peptidyl prolyl cis trans isomerase alpha, catalysis, isomerisation, prolyl peptide bond.
 .,
 ..
 Length 5;
 Indels
 0; Indels
 Length 5;
 Suzuki
 ..
 100.0%; Score 21; DB 5; 1 100.0%; Pred. No. 1.4e+06;
 DB 2; L
1.4e+06;
 Score 16; DB 2
Pred. No. 1.4e-
1; Mismatches
 Mismatches
 Takahashi N,
 Saccharomyces cerevisiae; strain AH22.
 Example 2; Page 23; 85pp; English.
 AAR72928 standard; peptide; 5 AA.
 Yeast PPIase tryptic fragment 8.
 ;
 89JP-00184738.
89JP-00260244.
89JP-00344705.
90EP-00307914.
 94EP-00203612
 Hayano I, Katou S, Maki N,
 76.2%;
75.0%;
 (first entry)
 Query Match
Best Local Similarity 75.0
Matches 3; Conservative
 5; Conservative
 (revised)
 WPI; 1995-140756/19
 Query Match
Best Local Similarity
```

(first entry)

29-NOV-1995

```
·;
 AAR72921-29 are tryptic fragments of a yeast PPIase (peptidyl prolyl cistrans isomerase). The yeast PPIase has a single mol. wt. of about 17 kba and a single isoelectric point of about 6.2. The enzyme catalyses the isomerisation of prolyl peptide bonds in proteins and accelerates the folding of the protein. The inventors are claiming a PPIase-beta. (Updated on 25-MAR-2003 to correct PW field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
 New E.coli peptidyl prolyl cis trans isomerase beta - used to accelerate the folding of proteins, partic. for activation of inactive recombinant
 Gaps
 Escherichia coli, protein conformation, folding, acceleration, PPIase-alpha, peptidyl prolyl cis trans isomerase alpha, catalysis; isomerisation, prolyl peptide bond.
 0;
 Score 16; DB 2; Length 5; Pred. No. 1.4e+06; 1; Mismatches 0; Indels
 Suzuki M;
 Takahashi N,
 on 16-OCT-2003 to standardise OS field)
 Saccharomyces cerevisiae; strain AH22.
 Example 2; Page 23; 85pp; English.
 AAR72884 standard; peptide; 5 AA.
 AAR72927 standard; peptide; 5 AA
 Yeast PPIase tryptic fragment 7.
 89JP-00184738.
89JP-00260244.
89JP-00344705.
 Maki N,
 76.2%;
75.0%;
 94EP-00203612
 90EP-00307914
 (revised)
(revised)
(first entry)
 3; Conservative
 Hayano T, Katou S,
 WPI; 1995-140756/19.
 Query Match
Best Local Similarity
Matches 3; Conserv
 (TOFU) TONEN CORP.
 2 VIAK 5
 2
 Sequence 5 AA;
|:|
WAK
 16-OCT-2003
25-MAR-2003
29-NOV-1995
 19-JUL-1990;
 19-JUL-1989;
06-OCT-1989;
 19-JUL-1990;
 16-OCT-2003
25-MAR-2003
 29-DEC-1989
 EP647714-A1
 AAR72884;
 AAR72927;
 proteins
 RESULT 5
 AAR72884
 AAR7292
 RESULT
 Ωp
 PRAKAKE
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0
 New E.coli peptidyl prolyl cis trans isomerase alpha - used to accelerate the folding of proteins, partic. for activation of inactive recombinant proteins.
 AAR72877-85 are tryptic fragments of a yeast PPIase (peptidyl prolyl cistrans isomerase). The yeast PPIase has a single mol. wt. of about 17 kDa and a single isoelectric point of about 6.2. The enzyme catalyses the isomerisation of prolyl peptide bonds in proteins and accelerates the folding of the protein. The inventors are claiming the PPIase-alpha. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to n16-OCT-2003 to standardise OS field)
 Gaps
 Escherichia coli, protein conformation, folding, acceleration, PPIase-alpha, peptidyl prolyl cis trans isomerase alpha, catalysis; isomerisation, prolyl peptide bond.
 0;
 Indels
 Peptide #4 used to enhance cellular adherence and growth.
 Length 5;
 Suzuki M;
 76.2%; Score 16; DB 2; Le
75.0%; Pred. No. 1.4e+06;
tive 1; Mismatches 0;
 Cellular adhesion; growth; expression; secretion
 Takahashi N,
 Saccharomyces cerevisiae; strain AH22
 Example 2; Page 23; 85pp; English.
 ¥
 Yeast PPlase tryptic fragment 8.
 AAO29981 standard; peptide; 5
 89JP-00260244.
89JP-00344705.
 19-NOV-2002; 2002WO-US037207.
 94EP-00203610.
 89JP-00184738
 Maki N,
 90EP-00307914
 (first entry)
 3; Conservative
 Hayano T, Katou S,
 Best Local Similarity
Matches 3; Conserv
 (TOFU) TONEN CORP.
 2 VIAK 5
 2 WAK 5
 WO2003044045-A2
 Sequence 5 AA;
 Unidentified
 19-JUL-1990;
 19-JUL-1989;
 06-OCT-1989;
29-DEC-1989;
 19-JUL-1990;
 03-SEP-2003
 EP647713-A1
 30-MAY-2003
 12-APR-1995
 AA029981;
 Query Match
 RESULT 6
 AA029981
à
 g
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The method is useful in quantifying the actual amount of 1
 WPI; 1989-294357/41.
 Best Local Similarity
Matches 3; Conserv
 Local Similarity
 1 SVIAK 5
 1 SVIAK 5
 SVVVK 5
 AVIAR 5
 Sequence 5 AA;
 Sequence 5 AA;
 Knauseder F,
 08-APR-1988;
 07-APR-1989;
 13-JUL-1988;
08-SEP-1988;
 29-JUL-1992
 11-OCT-1989
 EP336446-A
 AAP97806;
 Query Match
 Query Match
 Best Loc
Matches
 RESULT 9
 RESULT 8
 AAP97806
 8899998888
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0
 The invention relates to peptides having cell adhesion, growth, expression or secretion-enhancing activities. The peptides of the invention are useful for enhancing cell growth and/or secretion in a cell culture system. The present sequence is a peptide used to enhance
 Determining the actual amount of a polypeptide in a sample by measuring the amount of a cleavage product released from the polypeptide and using an exogenous polypeptide corresponding to the cleavage product as a
 peptide, useful for enhancing cell growth and/or secretion in a cell
 The present invention relates to a method of determining the actual amount of 1 or more selected polypeptides in a sample, which comprises releasing specific cleavage products from each of the polypeptides with cleavage agents and determining the actual amount of the product by comparison to a defined amount of a corresponding exogenous polypeptide (the actual amount of each of the cleavage products is directly related to the actual amount of the selected polypeptide from which it was
 Gaps
 ..
 Haaland PD;
 0; Indels
 76.2%; Score 16; DB 6; Length 5; 75.0%; Pred. No. 1.4e+06; ive 1; Mismatches 0; Indels
 Polypeptide quantitation; amount of protein; rat; human; purinergic receptor; P2X3.
 Wilkins JH,
 Rat purinergic receptor P2X3 peptide #2
 g
 Disclosure; Page 7; 26pp; English.
 Spargo
 ABR63446 standard; peptide; 5 AA.
 Claim 3; Page 44; 78pp; English.
 (BECT) BECTON DICKINSON & CO.
 cellular adherence and growth
 19-NOV-2001; 2001US-00992124.
 27-NOV-2002; 2002WO-US038334.
 29-NOV-2001; 2001US-0334325P.
 (THER-) THERMO FINNIGAN LLC
 (first entry)
 Heidaran M,
 Conservative
 Barnidge DR, Lindall AW;
 WPI; 2003-482396/45
 WPI; 2003-505195/47.
 Best Local Similarity
 Ŋ
 2 VIAK 5
 WO2003046148-A2.
 culture system
 Sequence 5 AA;
 VVAK
 Campbell RL,
 08-SEP-2003
 05-JUN-2003
 Rattus sp
 ABR63446;
 Query Match
 Matches
 New
 ABR63446
 RESULT
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0
 ö
 The inventors claim recombinant penicillin acyltransferase (PAT) and DNA coding for PAT. PAT catalyses the last step in the biosynthesis of penicillin G and penicillin V. More specifically, the coding strand of the DNA has the nucleotide sequence shown below. This includes three introns and codes for a PAT protein with mol. wt. ca. 40kD. Plasmid vectors pBC2001 and pBC2002 are specifically claimed
 Sequence of fragment 19, the tryptic fragment of recombinant penicillin acyltransferase (PAT) polypeptide 2.
 Gaps
 Gaps
more selected polypeptides in a sample, which may be important in research settings (e.g. in drug discovery and development) and in clinical settings (e.g. for medical diagnosis and for monitoring treatment efficacy). The present sequence is a peptide used to demonstrate the method of the invention
 Recombinant penicillin acyl-transferase - and DNA coding for it
 0;
 .,
 76.2%; Score 16; DB 7; Length 5; 60.0%; Pred. No. 1.4e+06; ive 1; Mismatches 1; Indels
 Score 15; DB 1; Length 5; Pred. No. 1.4e+06; 2; Mismatches 0; Indels
 Weber G;
 Penicillin biosynthesis; enzyme; antibiotic.
 Palma N,
 AAP97806 standard; protein; 5 AA.
 Claim 9; Page 48; 52pp; English.
 88AT-00000922.
88AT-00001806.
88AT-00002201.
 89EP-00106214.
 71.4%;
60.0%;
 Leitner E,
 Conservative
 3; Conservative
 Penicillium chrysogenum
 (BIOC) BIOCHEMIE GMBH
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Sequence 5 AA;
 Homo sapiens
 01-OCT-1998;
 WO9918208-A1
 02-OCT-1997;
 02-0CT-1997
02-0CT-1997
 02-0CT-1997
02-0CT-1997
 15-APR-1999
 02-OCT-1997
 02-OCT-1997
02-OCT-1997
 02-OCT-1997
 Ferrie AM,
 Duan DR,
 RESULT 11
 AAP91629
a
 ..
0
 New de-acetylase specific for L-N-acetyl-phosphinothricin - isolated from soil microbes, useful for stereoselective prodn. of L-phosphinothricin and for making male-sterile plants.
 οŧ
 The deacetylase has a molecular weight of 20000-100000, an optimum pH of.5-9.5 and substrate specificity for L-N-acetylphosphinothricin (L-AcPFT). It may be used for the deacetylation of AcPFT for the steroselective production of L-phosphinothricin (PPT) and for inducing reversible male serility in plants (PPT inhibits the enzyme glutamine synthase in anthers). The deacetylase comprises at least one of four sequences (See AARG1321-24). (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
 Human, secreted protein, treatment, prevention, protein therapy, AIDS, gene therapy, diagnosis, cancer, tumour; neurodegenerative disorder, developmental abnormality, fetal deficiency, blood disorder, leukemia,
 Gaps
 Deacetylase, enzyme; L-N-acetylphosphinothricin; L-AcPPT;
L-phosphonothricin; PPT; glutamine synthase; plant; male sterility;
 .
0
 66.7%; Score 14; DB 2; Length 4; 75.0%; Pred. No. 1.4e+06; ive 1; Mismatches 0; Indels
 Human secreted protein fragment #3 encoded from gene 41.
 Nocardia globerula; (mixed culture).
Cellulosimicrobium cellulans; (mixed culture).
 Agrobacterium tumefaciens; (mixed culture)
 (mixed culture).
; (mixed culture).
 AAY07986 standard; protein; 5 AA
AAR61324 standard; peptide; 4 AA
 Fragment of deacetylase enzyme.
 93DE-04308061.
 93DE-04308061.
 Claim 5; Page 5; 5pp; German.
 (first entry)
 (first entry)
 Conservative
 Variovorax paradoxus; (m
Brevundimonas diminuta;
 (revised)
 Schulz A, Bartsch K;
 WPI; 1994-286683/36.
 Best Local Similarity
Matches 3; Conserv
 (FARH) HOECHST AG.
 4
 2 VIAK 5
 |-|
VMAK
 Sequence 4 AA;
 DE4308061-A1.
 13-MAR-1993;
 06-JUL-1999
 16-OCT-2003
25-MAR-2003
 27-APR-1995
 L5-SEP-1994
 AAY07986;
 AAR61324;
 Query Match
 anther
 RESULT 10
 AAY07986
ID AAYC
XX AC AAYC
XX DT 06-1
XX
DE Hum
XX
XX Hum
XX
KW Gen
KW Gen
KW Gen
```

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0
immune system disease; autoimmune disease; hepatic disease; lymphoma; renal disease; inflammation; allery; Allerhimer's disease; schizophrenia; cognitive disorder; prostate disease; skeletal; cardiac; muscle disorder; pulmonary disorder; transplant rejection; osteoclast; osteoporosis;
 This invention describes novel isolated human genes and the secreted proteins they encode. The products of the invention are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polymorlectides. Specific uses are described for each of the 101 polymorlectides, which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, leukemias, diseases of the immune system,
 autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, prostate disease, skeletal or cardiac muscle disorders, pulmonary disorders,
 transplant rejection, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, digestive/endocrine disorders, infections and AIDS. The human secreted proteins of the invention are represented in AAY07852-Y07993 and the encoding nucleic acids are
 Gaps
 Young P;
A, Feng P
 New isolated human genes and the secreted polypeptides they encode
 0
 Greene JM, You
, Endress GA,
 Length 5;
 Indels
 arthritis; malignancy; digestive; endocrine; infection.
 Score 14; DB 2; Le
Pred. No. 1.4e+06;
3; Mismatches 0;
 Ruben SM, G
Carter KC,
 Disclosure; Page 344; 368pp; English
 Florence KA, Rosen CA, , Yu G, Janat F, Ni J,
 AAP91629 standard; protein; 4 AA.
 3;
 represented in AAX37451-X37552
 97US-0060862P.
97US-0060866P.
97US-0060874P.
 97US-0060837P.
97US-0060838P.
97US-0060839P.
97US-0060843P.
 66.7%;
40.0%;
 97US-0060884P
 98WO-US020775
 -0060880P
 (HUMA-) HUMAN GENOME SCI INC
 Conservative
 WPI; 1999-264022/22.
 Ferrie AM, Yu G, .
Lafleur DW, Shi Y;
 Query Match
Best Local Similarity
 1 SVIAK 5
 S
 SMVSK
```

AAP91629;

Synthetic.

```
The present sequence represents an immunisation motif normally excluded, but which may be used with advantage for tolerisation by itself or in conjunction with other epitope sequences from the present invention. The present invention describes a polypeptide comprising a human myelin basic protein (HMBP) fragment including P89-101 of HMBP, excluding native HMBP. The term P89-101 is not defined but may be intended to mean amino acids 89-101 of HMBP. The polypeptide can be used for tolerising a mammalian host immune system comprising B and T cells to an immunogen of interest, wherein said immunogen is restricted by a transplantation antigen of said
 and DNA
 The inventors claim recombinant penicillin acyltransferase (PAT) and DN coding for PAT. PAT catalyses the last step in the biosynthesis of penicillin G and penicillin V. More specifically, the coding strand of the DNA has the nucleotide sequence shown below. This includes three introns and codes for a PAT protein with mol. wt. ca. 40kD. Plasmid vectors pBC2001 and pBC2002 are specifically claimed
 Myelin basic protein; immunity; immune response; neurological; T-cell; human; immunogen; B-cell; transplantation antigen; immunomodulator.
 Polypeptide comprising human myelin basic protein fragment - useful as
 Gaps
 ţţ.
 0;
 Recombinant penicillin acyl-transferase - and DNA coding for
 0; Indels
 Length 4;
 61.9%; Score 13; DB 1; Le
100.0%; Pred. No. 1.4e+06;
tive 0; Mismatches 0;
 ö
 Immunisation motif associated with AChR 1.
 Weber
 (STRD) UNIV LELAND STANFORD JUNIOR
 Palma N,
 AAW55770 standard; peptide; 4 AA.
 Disclosure, Page 8; 8pp; English.
 Claim 9; Page 48; 52pp; English.
 97EP-00106788.
 87US-00086694
88EP-00307608
 (first entry)
 ы
 Conservative
(BIOC) BIOCHEMIE GMBH
 Zamvil S;
 Leitner
 (revised)
 WPI; 1989-294357/41.
 WPI; 1998-034664/04
 Query Match
Best Local Similarity
 immuno modulator
 3 IAK 5
 2 IAK 4
 Sequence 4 AA;
 Knauseder F,
 Unidentified
 17-AUG-1988;
 17-AUG-1987;
 17-AUG-1988;
 Steinman L,
 25-MAR-2003
08-JUL-1998
 EP805162-A1.
 05-NOV-1997.
 3;
 AAW55770;
 Matches
 RESULT 13
 AAW55770
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 Motif useful in tolerization alone or in association with epitopes to the
 Sequences will normally be part of 9-15 amino acid sequence, excluded as motifs for immunisation but useful in tolerisation. . (Updated on 25-WAR-2003 to correct PR field.) (Updated on 25-WAR-2003 to correct PR field.) (Updated on 25-WAR-2003 to correct PI field.)
 Oligopeptide and polypeptide compsns. - based on the amino acid sequence of an immunogen and used for modulating the immune system.
 Sequence of fragment 21, the tryptic fragment of recombinant penicillin acyltransferase (PAT) polypeptide 2.
 Gaps
 Autoantigen, MBP, myelin basic protein, transplantation antigen, myasthenia gravis; myasthenics; Transplantation antigen.
 0;
 Score 13; DB 1; Length 4; Pred. No. 1.4e+06; 2; Mismatches 0; Indels
 Penicillin biosynthesis; enzyme; antibiotic.
 (STRD) UNIV LELAND STANFORD JUNIOR.
 AAP97808 standard; protein; 4 AA
 Disclosure; Page; 7pp; English.
 88AT-00000922.
88AT-00001806.
88AT-00002201.
 88EP-00307608
 89EP-00106214
 87US-00086694
 Query Match
Best Local Similarity 50.0%;
Matches 2; Conservative
 (first entry)
 (first entry)
 acetyl choline receptor
 Penicillium chrysogenum
 Zamvil S;
 (revised)
 WPI; 1989-055696/08.
 ::||
LVAK 4
 2 VIAK 5
 Sequence 4 AA;
 17-AUG-1988;
 17-AUG-1987;
 29-JUL-1992
 07-APR-1989;
 13-JUL-1988;
08-SEP-1988;
 08-APR-1988
 25-MAR-2003
09-JUL-1990
 22-FEB-1989.
 11-0CT-1989
 Steinman L,
 EP304279-A.
 EP336446-A
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AAP97808;

RESULT 12 AAP97808

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ABR57300 standard; peptide; 4
 09-SEP-2003
 12-JUN-2003
 ABR57300;
 Query Match
 Best Loc
Matches
 RESULT 15
 Dp
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0
 immune system, and for treating multiple sclenosis comprising administering a peptide derived from hMBP (human myelin basic protein). The peptide induces an autoimmune response (T cell) to a self-antigen (or part of it), and binds to an MHC (major histocompatibility complex) antigen of a host susceptible to autoimmune diseases, i.e. competes with binding to MBP and inhibit proliferation of MBP-reactive cells. The peptide has immunosuppressive and neuroprotective activity. This sequence represents a peptide derived from the human MBP protein which can be used
 Modulating or tolerizing the immune system, useful for treating multiple sclerosis, by administering a peptide derived from human myelin binding protein.
 This invention describes a novel method for modulating or tolerizing the
host. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
 Gaps
 ;
 multiple sclerosis; autoimmune response; autoimmune disease; immunosuppressive; neuroprotective.
 protein; human; tolerance; immune system;
 Score 13; DB 2; Length 4;
Pred. No. 1.4e+06;
2; Mismatches 0; Indels
 Human MBP protein derived peptide SEQ ID 33
 2; Mismatches
 Disclosure; Page 14; 21pp; English.
 ABB84333 standard; peptide; 4 AA.
 89US-00379500.
90US-00517245.
91WO-US002991.
92US-00877444.
 61.9%;
 95US-00484409
 87US-00086694
 93US-00066325
 93US-00125407
 (first entry)
 Query Match
Best Local Similarity 50.v.
 Zamvil S;
 WPI; 2002-598709/64
 STEINMAN L.
 MBP; myelin basic
 ZAMVIL S.
 ::||
1 LVAK 4
 for tolerization
 US2002076412-A1.
 2 VIAK 5
 Sequence 4 AA;
 Sequence 4 AA;
 Homo sapiens
 07-JUN-1995;
 17-0CT-2002
 Steinman L,
 20-JUN-2002
 01-MAY-1990
 01-MAY-1991
 30-APR-1992
 21-MAY-1993
 22-SEP-1993
 ABB84333;
 (STEI/)
 ZAMV/)
 RESULT 14
 ABB84333
 S S S S
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0
 The present invention describes an isolated nucleic acid (1) encoding a nucleic acid polymerase or a derivative nucleic acid polymerase with a mucleic acid polymerase with a mutation that decreases 5.3' exonuclease activity or that reduces discrimination against dideoxynucleotide triphosphates. Also described: (1) a vector comprising the nucleic acid (1); (2) a host cell comprising the nucleic acid polymerase or its derivative; (4) a kit comprising a container containing the nucleic acid polymerase of (3); (5) making the nucleic acid polymerase of (3); (6) synthesising a DNA, (7) thermocyclic amplification of nucleic acid; and (8) primer extending a DNA. The nucleic acid (1) is useful for DNA sequencing or amplification, reverse transcription, RNA amplification or primer extension reactions. The present sequence represents a Thermus oshimai and cell contains and polymerase peptide, which is given in the exemplification of
 reverse
 Thermus oshimai nucleic acid polymerase peptide 704-707 SEQ ID NO:26.
 Gaps
 Thermus oshimai; nucleic acid polymerase; enzyme; DNA sequencing; amplification; reverse transcription; RNA amplification;
 New nucleic acid, useful for DNA sequencing or amplification, r
transcription, RNA amplification or primer extension reactions.
 0;
 Length 4;
 Indels
 61.9%; Score 13; DB 7; L6
100.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 0;
 Search completed: August 12, 2004, 06:53:04 Job time : 93 secs
 Disclosure; Page 32; 64pp; English.
 22-NOV-2002; 2002WO-US037764.
 30-NOV-2001; 2001US-0334798P.
 ن
..
(first entry)
 3; Conservative
 Rozzelle
 the present invention
 (APPL-) APPLERA CORP
 WPI; 2003-505286/47.
 Local Similarity
 primer extension.
 Thermus oshimai
 WO2003048310-A2
 Sequence 4 AA;
 3 IAK 5
 Bolchakova E,
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0

0; Gaps

0; Indels

Score 13; DB 5; Length 4; Pred. No. 1.4e+06; 2; Mismatches 0; Indels

Query Match
Best Local Similarity 50.0%;
Matches 2; Conservative

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August 12, 2004, 06:54:59; Search time 41 Seconds (without alignments) 38.284 Million cell updates/sec
 Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_BNW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_BNW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1292805 seqs, 313927144 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 - protein search, using
 US-09-890-463-1
21
 1 SVIAK 5
 Minimum DB seq length: 0 Maximum DB seq length: 5
 Title:
Perfect score:
 Scoring table:
 OM protein
 Database :
 Searched:
 Sequence:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |            | Description     | Sequence 4, Appli | Sequence 4, Appli | Sequence 8, Appli | Sequence 12, Appl | Sequence 16, Appl | Sequence 20, Appl | Sequence 24, Appl | Sequence 329, App | Sequence 4, Appli | Sequence 8, Appli | Sequence 12, Appl | Sequence 16, Appl | Sequence 20, Appl | 24,              | Sequence 4, Appli |
|-----------|------------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|
| SUMMARIES |            | QI              | US-09-992-124A-4  | US-09-862-145A-4  | US-09-862-145A-8  | US-09-862-145A-12 | US-09-862-145A-16 | US-09-862-145A-20 | US-09-862-145A-24 | US-10-195-730-329 | US-10-402-029-4   | US-10-402-029-8   | US-10-402-029-12  | US-10-402-029-16  | US-10-402-029-20  | US-10-402-029-24 | US-10-285-108A-4  |
|           |            | DB              | 10                | 10                | 10                | 10                | 10                | 10                | 10                | 14                | 15                | 72                | 15                | 15                | 15                | 15               | 16                |
|           |            | Match Length DB | D                 | Ŋ                 | 5                 | 5                 | Ŋ                 | 5                 | Ŋ                 | Ŋ                 | S                 | S                 | J.                | 2                 | S                 | 2                | 2                 |
|           | *<br>Query | Match           | 76.2              | 66.7              | 66.7              | 66.7              | 66.7              | 66.7              | 66.7              | 66.7              | 66.7              | 66.7              | 66.7              | 66.7              | 66.7              | 66.7             | 66.7              |
|           |            | Score           | 16                | 14                | 14                | 14                | 14                | 14                | 14                | 14                | 14                | 14                | 14                | 14                | 14                | 14               | 14                |
|           | Result     | No.             | 1                 | 7                 | n                 | 4                 | 2                 | 9                 | 7                 | œ                 | σ                 | 10                | 11                | 12                | 13                | 14               | 15                |

| 8, 7<br>12,<br>16,<br>20,                                                    | Sequence 24, Appl<br>Sequence 33, Appl<br>Sequence 26, Appl<br>Sequence 17, Appl                  | 3, Ag<br>31, 7<br>38, 7<br>163,                                             | 3, 4, 11,                                        | Sequence 8, Appli<br>Sequence 6, Appli<br>Sequence 2, Appli<br>Sequence 6, Appli<br>Sequence 18, Appli                | 20, 7<br>50, 7<br>50, 7<br>30, 7                                                            | 3.78<br>e 3.78                                                                                |
|------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------|--------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------|
| US-10-285-108A-8<br>US-10-285-108A-1<br>US-10-285-108A-1<br>US-10-285-108A-2 | 5 16 US-10-285-108A-24<br>4 8 US-08-484-409-33<br>4 14 US-10-303-109A-26<br>5 14 US-10-197-927-17 | US-09-797-543-3<br>US-09-359-325A-3<br>US-09-945-249-38<br>US-09-870-759-16 | -09-751-7<br>-10-371-4<br>-10-016-7<br>-10-033-0 | 4 13 US-10-078-458-8<br>4 14 US-10-087-905-6<br>4 14 US-10-287-639-2<br>4 UT US-10-087-942-6<br>4 14 US-10-083-994-18 | 1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1<br>1 | 5 9 US-00-748-114-28<br>5 9 US-09-945-249-37<br>5 10 US-09-992-124A-3<br>5 10 US-09-562-912-4 |
| 0000                                                                         | 14 66.7<br>13 61.9<br>13 61.9<br>13 61.9                                                          |                                                                             |                                                  | 12 57.1<br>12 57.1<br>12 57.1<br>12 57.1                                                                              |                                                                                             | 12 57.1<br>12 57.1<br>12 57.1<br>12 57.1                                                      |
| 16<br>117<br>19                                                              | 22 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3                                                            | 22 2 2 4 4 5 4 5 4 5 5 5 5 5 5 5 5 5 5 5                                    | 3 3 3 8<br>3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3       |                                                                                                                       | ა დ დ 4 4<br>- ფ დ O L                                                                      | 4 4 4 4<br>2 4 4 3                                                                            |

#### ALIGNMENTS

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 APPLICANT: Heidaran, Mohammad A.
APPLICANT: Heidaran, Mohammad A.
APPLICANT: Haland, Perry D.
APPLICANT: Wilkins, Jamie H.
APPLICANT: Spargo, Catherine A.
APPLICANT: Campbell, Robert L.
TITLE OF INVENTION: Peptides Promoting Cell Adherence, Growth and Secretion FILE REPREBUCE: 102-410
CURRENT APPLICATION NUMBER: US/09/992,124A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 70
 Gaps
 ; FEATURE:
; OTHER INFORMATION: Synthetic peptide selected for biological activity
US-09-992-124A-4
 0;
 Length 5;
 Indels
 Ouery Match 76.2%; Score 16; DB 10; L. Best Local Similarity 75.0%; Pred. No. 1.2e+06; Matches 3; Conservative 1; Mismatches 0;
 Sequence 4, Application US/09992124A Publication No. US20030162289A1 GENERAL INFORMATION:
 Sequence 4, Application US/09862145A; Publication No. US20030138388A1; GENERAL INFORMATION:
 NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
 ORGANISM: artificial sequence
 2 VIAK 5
 2 VVAK
 RESULT 2
US-09-862-145A-4
US-09-992-124A-4
 SEQ ID NO 4
LENGTH: 5
 TYPE: PRT
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US-09-862-145A-12
 US-09-862-145A-16
 US-09-862-145A-20
 LENGTH: 5
 TYPE: PRT
 FEATURE:
 Best Loc
Matches
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0
 APPLICANT: Shapiro, Stanley
TITLE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin
FILE REFERENCE: J&J-1991
 APPLICANT: Stablerg, Miri
APPLICANT: Shapiro, Stanley
TITLE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin
FILE REFERENCE: J&J-1991
CURRENT APPLICATION NUMBER: US/09/862,145A
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
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 Sequence 8, Application US/09862145A
Publication No. US203013838BA1
GENERAL INFORMATION:
APPLICANT: Seiberg, Miri
APPLICANT: Seiberg, Stanley
TITLE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin
FILE REFERENCE: J&J-1991
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 66.7%; Score 14; DB 10; Length 5; 60.0%; Pred. No. 1.2e+06;
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 1; Indels
 1; Indels
 Score 14; DB 10;
Pred. No. 1.2e+06;
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 CURRENT APPLICATION NUMBER: US/09/862,145A CURRENT FILING DATE: 2001-05-21 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin version 3.1 SEQ ID NO 4
 CURRENT APPLICATION NUMBER: US/09/862,145A
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 24
SOFWARE: Patentin version 3.1
SEQ ID NO 8
 NAME/KEY: MISC_FEATURE

1. DCATION: (5)..(5)

OTHER INFORMATION: C-terminal Amidation

US-09-862-145A-4
 ; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-862-145A-8
 OTHER INFORMATION: Synthetic Peptide
 Sequence 12, Application US/09862145A Publication No. US20030138388A1 GENERAL INFORMATION:
 66.7%; Scur
60.0%; Pred
1;
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 3; Conservative
 Query Match
Best Local Similarity 60.0
Matches 3; Conservative
APPLICANT: Seiberg, Miri
 Best Local Similarity
Matches 3; Conserv
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SLIGK 5
 1 SVIAK 5
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1 SLIGK 5
 RESULT 4
US-09-862-145A-12
 RESULT 3
US-09-862-145A-8
 Query Match
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 LENGTH:
 LENGTH:
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 Sequence 20, Application US/09862145A
| Sequence 20, Application No. US20030138388A1
| GENERAL INFORMATION:
| APPLICANT: Selberg, Miri
| APPLICANT: Shapiro, Stanley
| TITLE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin FILE REPRENCE: US/09/862,145A
| CURRENT APPLICATION NUMBER: US/09/862,145A
| CURRENT FILING DATE: 2001-05-21
| NUMBER OF SEQ ID NOS: 24
| SEQ ID NO 20
| LENGTH: 5
 APPLICANT: Seiberg, Miri
APPLICANT: Shapiro, Stanley
TILLE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin
FILE REFERENCE: UKJ-1991.
CURRENT APPLICATION NUMBER: US/09/862,145A
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 5
 Gaps
 Gaps
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 .;
 66.7%; Score 14; DB 10; Length 5; 60.0%; Pred. No. 1.2e+06; 1; Mismatches 1; Indels
 66.7%; Score 14; DB 10; Length 5; 60.0%; Pred. No. 1.2e+06; 1; Mismatches 1; Indels
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 LOCATION: (5). 7(5)
OTHER INFORMATION: Amidated C-terminus
 OTHER INFORMATION: Synthetic Peptide
 OTHER INFORMATION: Synthetic Peptide
 Sequence 16, Application US/09862145A; Publication No. US20030138388A1
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 ORGANISM: Artificial Sequence
 3; Conservative
 3; Conservative
 FEATURE:
NAME/KEY: MISC_FEATURE
 Query Match
Best Local Similarity
Matches 3; Conserv
 Query Match
Best Local Similarity
 GENERAL INFORMATION:
 1 SVIAK 5
 1 SLIGK 5
 1 SVIAK 5
 SLIGK 5
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Gaps

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66.7%; Score 14; DB 15; Length 5; 60.0%; Pred. No. 1.2e+06; tive 1; Mismatches 1; Indels
 GENERAL INFORMATION:
APPLICANT: Lin, Connie
APPLICANT: Lin, Connie
APPLICANT: Seibergy Miri
TITLE OF INVENTION: Compositions for Darkening the Skin
FILE REFERENCE: J&J-2099
CURRENT PALLIANION NUMBER: US/10/402,029
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 5
 DB 15; Length 5;
 Score 14; DB 14; Length 5; Pred. No. 1.2e+06;
 0; Indels
 GENERAL INFORMATION:
APPLICANT: Lin, Connie
APPLICANT: Seiberg, Min.
TITLE OF INVENTION: Compositions for Darkening the Skin
FILE REFERENCE: J&J-2099
CURRENT APPLICATION NUMBER: US/10/402,029
CURRENT PILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
 3; Mismatches
 66.7%; Score 14;
 NAME/KEY: MISC FEATURE
LOCATION: (5)...(5)
COTHER INFORMATION: C-terminal Amidation
US-10-402-029-4
 ; OTHER INFORMATION: Synthetic Peptide US-10-402-029-8
 OTHER INFORMATION: Synthetic Peptide
 Sequence 8, Application US/10402029
Publication No. US20040005288A1
 Sequence 4, Application US/10402029
Publication No. US20040005288A1
 ORGANISM: Artificial Sequence
 66.7%;
 TYPE: PRT ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 390
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 329
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Best Local Similarity 40.03
Matches 2; Conservative
 Query Match 66.7
Best Local Similarity 60.0
Matches 3; Conservative
 TYPE: PRT
CRGANISM: Homo sapiens
US-10-195-730-329
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1 SMVSK 5
 1 SVIAK 5
 1 SVIAK 5
 1 SLIGK 5
 US-10-402-029-8
 US-10-402-029-4
 TYPE: PRT
 SEQ ID NO 4
 Query Match
 FEATURE:
 FEATURE:
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 RESULT 10
 RESULT 9
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 US-09-862-145A-24
US-09-862-145A-24

Delication No. US2003013838A1

Publication No. US2003013838A1

GENERAL INFORMATION:

APPLICANT: Sciberg, Miri

APPLICANT: Sciberg, Miri

APPLICANT: Shapiro, Stanley

ITILE OF INVENTION: Peptides and the Use Thereof in Darkening the Skin

FILE REBERENCE: US-1991

CURRENT APPLICATION WOMBER: US/09/862,145A

CURRENT PILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 24

SOFFWARE: Patentin version 3.1

SEQ ID NO 24

LENGTH: 5
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 66.7%; Score 14; DB 10; Length 5; 60.0%; Pred. No. 1.2e+06; cive 1; Mismatches 1; Indels
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 Sequence 329, Application US/10195730
Publication No. US20030144492A1
GENERAL INFORMATION:
APPLICANT: Rosen et. al
TITLE OF INVENTION: 101 Human Secreted Proteins
 CHER INPORMATION: Stearatoyl N-terminus US-09-862-145A-24
 FILE REFERENCE: PZ017P1
CURRENT APPLICATION NUMBER: US/10/195,730
CURRENT FILING DATE: 2002-07-16
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 NAME/KEY: MISC_FEATURE

CCATION: (5)..(5)

CTHER INFORMATION: Stearatoyl C-terminus
US-09-862-145A-20
 PRIOR APPLICATION NUMBER: US/09/281,976
PRIOR FILING DATE: 1999-03-31
PRIOR FILING DATE: 1997-10-02
PRIOR PAPLICATION NUMBER: 60/060,837
PRIOR PLING DATE: 1997-10-02
PRIOR PLING DATE: 1997-10-02
 OTHER INFORMATION: Synthetic Peptide
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 ORGANISM: Artificial Sequence
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3; Conservative
 Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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SLIGK 5
 |:| |
1 SLIGK 5
 1 SVIAK 5
 1 SVIAK 5
 RESULT 8
US-10-195-730-329
 TYPE: PRT
 FEATURE:
 FEATURE:
 FEATURE:
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Gaps

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Gaps
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 Length 5;
 Length 5;
 Indels
 APPLICANT: Lin, Connie
APPLICANT: Seiberg, Miri
TITLE OF INVENTION: Compositions for Darkening the Skin
FITLE OF INVENTION: Compositions for Darkening the Skin
FILE REFERENCE: J64-2099
CURRENT APPLICATION NUMBER: US/10/402,029
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 5
 APPLICANT: Lin, Connie
APPLICANT: Lin, Connie
TITLE OF INVENTION: Compositions for Darkening the Skin
FILE REFERENCE: J&J-2099
CURRENT APPLICATION NUMBER: US/10/402,029
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 30
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LENGTH: 5
 66.7%; Score 14; DB 15;
60.0%; Pred. No. 1.2e+06;
iive 1; Mismatches 1;
 Query Match

66.7%; Score 14; DB 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 1.
 Mismatches
 NAME/KEY: MISC FEATURE
LOCATION: (1)._(1)
OTHER INFORMATION: Stearatoyl N-terminus
 PEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)...(1)
CATHER INDERMATION: Stearatoyl N-terminus
US-10-402-029-24
 ; LOCATION: (5)...(5); OTHER INFORMATION: Amidated C-terminus US-10-402-029-20
 OTHER INFORMATION: Synthetic Peptide
 OTHER INFORMATION: Synthetic Peptide
 ; Sequence 20, Application US/10402029
; Publication No. US20040005288A1
; GENERAL INFORMATION:
 Sequence 24, Application US/10402029; Publication No. US20040005288A1; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 3; Conservative
 Conservative
 NAME/KEY: MISC_FEATURE
 Best Local Similarity
Matches 3; Conser
 1 SVIAK 5
 1 SVIAK 5
 1 SLIGK 5
 SLIGK
 US-10-402-029-20
 US-10-402-029-24
 Query Match
 TYPE: PRT
 FEATURE:
 Matches
 RESULT 14
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 Gaps
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 Length 5;
 60.0%; Pred. No. 1.2e+06;
live 1; Mismatches 1; Indels
 RESULT 12
US-10-402-029-16
| Sequence 16. Application US/10402029
| Publication No. US20040005288A1
| GENERAL INFORMATION:
| APPLICANT: Lin, Comnie
| APPLICANT: Lin, Compositions for Darkening the Skin TITLE OF INVENTION: Compositions for Darkening the Skin FILE REFERENCE: UsJ-2099
| CURRENT FILING DATE: 2003-03-28
| NUMBER OF SEQ ID NOS: 30
| SOOFTHARE: PatentIn version 3.1
 66.7%; Score 14; DB 15; Length 5; 60.0%; Pred. No. 1.2e+06; Live 1; Mismatches 1; Indels
 APPLICANT: Lin, Connie
APPLICANT: Lin, Connie
APPLICANT: Seiberg, Miri
TITLE OF INVENTON: Compositions for Darkening the Skin
FILE REFERENCE: J&c-2099
CURRENT APPLICATION NUMBER: US/10/402,029
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
 Score 14; DB 15;
Pred. No. 1.2e+06;
 LOCATION: (1). (1) OTHER INFORMATION: Palmitoyl N-terminus
 ; NAME/KEY: MISC_FEATURE
; LOCATION: (1)...(1)
; CTHER INFORMATION: Palmitoyl N-terminus
US-10-402-029-16
 NAME/KEY: MISC_FEATURE
LOCATION: (5)._(5)
CTHER INFORMATION: Amidated C-terminus
US-10-402-029-12
 OTHER INFORMATION: Synthetic Peptide
 OTHER INFORMATION: Synthetic Peptide
 ; Sequence 12, Application US/10402029
; Publication No. US20040005288A1
; GENERAL INFORMATION:
 66.7%;
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 3; Conservative
 3; Conservative
 NAME/KEY: MISC FEATURE
Best Local Similarity
Matches 3; Conserv
 Best Local Similarity
 Best Local Similarity
 1 SVIAK 5
 SLIGK 5
 1 SVIAK 5
 1 SLIGK 5
 RESULT 11
US-10-402-029-12
 SEQ ID NO 12
 SEQ ID NO 16
 Query Match
 Query Match
 FEATURE:
 FEATURE:
 LENGTH
 Matches
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0;
 RESULT 15
US-10-285-108A-4

j Sequence 4, Application US/10285108A

j Sequence 4, Application US/10285108A

j GENERAL INFORMATION:

j APPLICANT: Lin, Connie

APPLICANT: Mu, Jane

TITLE OF INVENTION: Compositions for Darkening the Skin and/or Hir

FILE REPERBACE: J&J-217

CURRENT APPLICATION WUMBER: US/10/285,108A

CURRENT FILING DATE: 2002-10-31

CURRENT FILING DATE: 2002-10-31

SOFTWARE: PATENT:

LENGTH: 5

LENGTH: 5

TYPE: PATENT:

CORGANISM: Artificial Sequence

FEATURE:

FEATURE:

COCATION: (5). (5)

COCATION: (5). (5)

COCATION: (5). (5)

COCATION: (5). (5)

US-10-285-108A-4
 Gaps
 ;
 Query Match
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels
1 SVIAK 5
|:| |
1 SLIGK 5
 Dp
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Search completed: August 12, 2004, 07:02:19 Job time : 41 secs

1 SVIAK 5 |:| | 1 SLIGK 5

g

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2004, 06:55:24; Search time 50 Seconds (without alignments) 96.066 Million cell updates/sec Run on:

US-09-890-463-2 83 Title: Perfect score:

1 SVIAKQMTYKVYMSGTV 17 Sequence:

**BLOSUM62** Scoring table: 1586107 segs, 282547505 residues Searched:

Gapop 10.0 , Gapext 0.5

470470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 17

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\* Database

geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp201s:\*
geneseqp2033s:\*
geneseqp2033s:\* geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

|               |       | ф              |        |    | SUMMAKIES |             |           |
|---------------|-------|----------------|--------|----|-----------|-------------|-----------|
| Result<br>No. | Score | Query<br>Match | Length | DB | ID        | Description |           |
|               | 83    | 100.0          | 17     |    | AAY97148  | Aay97148    | Pigment p |
| 7             | 73    | 88.0           | 1      | 2  | ABB99066  | Abb99066    | N-termina |
| m             | 72    | 86.7           | 16     | Ŋ  | ABB99073  | Abb99073    | N-termina |
| 4             | 70    | 84.3           | 16     | ហ  | ABB99072  | Abb99072    | N-termina |
| 2             | 69    | 83.1           |        | Ŋ  | ABB99068  | Abb99068    | N-termina |
| 9             | 69    | 83.1           | +1     | ß  | ABB99070  | Abb99070    | N-termina |
| 7             | 68    | 81.9           | П      | Ŋ  | ABB99067  | Abb99067    | N-termina |
| œ             | 67    | 80.7           | 16     | ഹ  | ABB99071  | Abb99071    | N-termina |
| 6             | 99    | 79.5           |        | Ŋ  | ABB99069  | Abb99069    | N-termina |
| 10            | 62    | 74.7           | 16     | Ŋ  | ABB99074  | Abb99074    | N-termina |
| 11            | 36    | 43.4           |        | ហ  | ABP70008  | Abp70008    | Colour Fa |
| 12            | 29    | 34.9           | 14     | 7  | AAR77526  | Aar77526    | p45 metal |
| 13            | 29    | 34.9           | 14     | 7  | AAW05846  | Aaw05846    | Fusarium  |
| 14            | 29    | 34.9           | 15     | Ŋ  | AAM48968  | Aam48968    | Human zin |
| 15            | 28    | 33.7           | 11     | 7  | AAW39598  | Aaw39598    | Human mel |
| 16            | 28    | 33.7           | 12     | 4  | AAB45642  | Aab45642    | Vasoactiv |
| 17            | 28    | 33.7           | 13     | 7  | AAR69362  | Aar69362    |           |
| 18            | 28    | 33.7           | 13     | 4  | AAB45641  | Aab45641    | Vasoactiv |
| 19            | 28    | 33.7           | 13     | 4  | AAB45639  | Aab45639    |           |
| 20            | 28    | 33.7           | 1      | 2  | AAE19614  | Aae19614    | Human ste |
| 21            | 28    | 33.7           | 14     | 7  | AAR79549  | Aar79549    |           |
| 22            | 28    | 33.7           | 14     | 4  | AAB88179  | Aab88179    | CD66 pept |
| 23            | 28    | 33.7           | 14     | 4  | AAB45638  | Aab45638    |           |
| 24            | 28    | 33.7           | 14     | 4  | AAB45622  | Aab45622    | Vasoactiv |
| 25            | 28    | 33.7           | 15     | 7  | AAR79548  | Aar79548    | Analgesic |

| Aab99955 Human lat | AAD45619 VASOACLIV   |          | •        | Aay85708 Peptide s | Aab45618 Vasoactiv | Aab45620 Vasoactiv | Aar79546 Analgesic | Aab45617 Vasoactiv | Ada90426 MS-Roche | Ada89996 Anti-Abet | Abp19278 HIV B62 s | Abp19181 HIV B62 s | Abp21094 HIV A03 m | Abp23330 HIV All m | Abp21373 HIV A03 m | 4 HIV    | Add57378 HLA bindi | Add57758 HLA bindi |
|--------------------|----------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|
| AAB99955           | AAB45619<br>AAB45621 | ABG71317 | AAR79547 | AAY85708           | AAB45618           | AAB45620           | AAR79546           | AAB45617           | ADA90426          | ADA89996           | ABP19278           | ABP19181           | ABP21094           | ABP23330           | ABP21373           | ABP23124 | ADD57378           | ADD57758           |
| 4 4                | 4 4                  | ۲ LC     | ~        | m                  | 4                  | 4                  | ~                  | 4                  | 9                 | 9                  | 4                  | 4                  | 4                  | 4                  | 4                  | 4        | 7                  | 7                  |
| 15                 | 1.5<br>7.5           | 12       | 16       | 16                 | 16                 | 16                 |                    | 17                 | 17                | 17                 | 80                 | 80                 | Q                  | σv                 | σ                  | σ        | σ                  | σ                  |
| 33.7               | 33.7                 | 33.7     | സ        | 33.7               | 33.7               | 33.7               | 33.7               | 33.7               | 33.7              | 33.7               | 32.5               | 32.5               | 32.5               | 32.5               | 32.5               | 32.5     | 32.5               | 32.5               |
| 28                 | 7 C                  | 7 7 7    | 28       | 28                 | 28                 | 28                 | 28                 | 28                 | 28                | 28                 | 27                 | 27                 | 27                 | 27                 | 27                 | 27       | 27                 | 27                 |
| 26                 | / 7 C                | 0 00     | 3.0      | 31                 | 32                 | 33                 | 34                 | 35                 | 36                | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43       | 44                 | 45                 |

#### ALIGNMENTS

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The N-terminal peptides shown in AAV97147-48 are from pigment protein irradiation tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dyestuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters
 Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 N-terminal; pigment protein from coral tissue; PPCT; fluorescence; tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet;
 Pigment protein from coral tissue N-terminal peptide 2.
 AAY97148 standard; peptide; 17 AA
 Claim 4; Page 42; 49pp; English.
 99AU-00008463.
 02-FEB-2000; 2000WO-AU000056.
 ŝ
 (first entry)
 Hoegh-Guldberg O, Dove
 WPI; 2000-532892/48.
 (UNSY) UNIV SYDNEY
 Acropora horrida.
 WO200046233-A1.
 02-FEB-1999;
 04-DEC-2000
 10-AUG-2000
 tissue mar
 AAY97148;
RESULT 1
 AAY97148
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Sequence 17 AA; Query Match

100.0%; Score 83; DB 3; Length 17;

Length 16;

Sequence 16 AA;

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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a ransgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs embedded in a gel matrix improve image quality in situations of distorted light specira (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a colour-facilitating molecule (CFM)
 0
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 .
 0; Indels
 Dove SG;
 100.0%; Pred. No. 3.6e-08;
 Brugliera F, Mason J,
 N-terminal amino acid sequence of a CFM #6.
 Mismatches
 Claim 4; Page 280; 510pp; English.
 ABB99066 standard; peptide; 16 AA
 0;
 Prescott M;
 SVIAKOMTYKVYMSGTV 17
 1 SVIAKOMTYKVYMSGTV 17
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 02-MAR-2001; 2001US-0273227P
 (first entry)
 17; Conservative
 QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80.
 UV sink; sunscreen.
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENS
(JONE/) JONES E L.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
Best Local Similarity
 WO200270703-A2.
 Unidentified.
 22-JAN-2003
 12-SEP-2002.
 white light
 ABB99066;
 Matches
 RESULT 2
ABB99066
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The invention relates to an isolated colour-facilitating molecule (CFW)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extrameous

non-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing agent. Other

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

uses include transducing or intensifying an image, providing additional

light for growing photoropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

coating materials that experience W damage e.g. plastics and car

coating materials that experience molecules, photon traps, UV sinks or

the varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs modify visible colour in edible and/or ornamental

chugal species, and in fruits and vegetables to enhance their

marketability, CFMs embedded in a gel matrix improve image quality in

situations of distorted lights specira (blomatrix). The first all-protein

chromophore to be isolated was Green Fluorescent protein (GFP). The
 ·.
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule, CFM; green fluorescent protein; GFP; chromophore; blomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen.
 .
 Brugliera F, Mason J, Dove SG; Prescott M;
 Score 73; DB 5; I
Pred. No. 2.2e-06;
 N-terminal amino acid sequence of a CFM #13.
 Mismatches
 Claim 4; Page 281; 510pp; English.
 ABB99073 standard; peptide; 16 AA
 0 ;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 88.0%;
93.8%;
 01-MAR-2002; 2002WO-GB000928
 1 SVIATOMTYKVYMSGT 16
 22-JAN-2003 (first entry)
 1 SVIAKOMTYKVYMSGT
 Conservative
 QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80.
Query Match
Best Local Similarity
Matches 15; Conserv
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 (NUFA-) NUFARM LTD
 (JONE/) JONES E L.
 WO200270703-A2.
 UNIV
 Unidentified
 white light.
 12-SEP-2002
 ABB99073;
 (UYQU
 RESULT 3
 ABB99073
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The invention relates to an isolated colour-facilitating molecule (CFM)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human ey in the absence of excitation by extraneous

non-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing coloured plant

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

uses include transducing or intensifying an image, providing additional

light for growing phototropic organisms e.g. adjace and/or corals, for

coating materials that experience UV damage e.g. plastics and car

upholstery. CFMs are useful in the flower industry, in the development of

new varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs modify visible colour in edible and/or ornamental

fungal species, and in fruits and vegetables to enhance their
 ö
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP, chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
current sequence represents the N-terminal amino acid sequence of a
 ÷
 86.7%; Score 72; DB 5; Length 16; 93.8%; Pred. No. 3.4e-06; ive 0; Mismatches 1; Indels
 Dove SG;
 Mason J,
 N-terminal amino acid sequence of a CFM #12.
 Brugliera F,
Prescott M;
 Claim 4; Page 281; 510pp; English.
 colour-facilitating molecule (CFM)
 ABB99072 standard; peptide; 16 AA.
 01-MAR-2002; 2002WO-GB000928.
 02-MAR-2001; 2001US-0273227P.
 2001AU-00003874.
 15-OCT-2001; 2001US-0329816P
 1 SVIAKQMTYKVYMSGT 16
 SVIAKOMÍÝKVÝMSDÍ 16
 (first entry)
 15; Conservative
 OUEENSLAND.
 Karan M,
 WPI; 2002-740765/80.
 sink; sunscreen.
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENS
 Similarity
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 (JONE/) JONES E L.
 WO200270703-A2.
 Sequence 16 AA;
 21-MAR-2001;
 Unidentified
 22-JAN-2003
 12-SEP-2002,
 white light.
 ABB99072;
 Query Match
Best Local
 Matches
 ABB99072
 RESULT
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0;
 when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured flaece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholatery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include,
 The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell
marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 .;
0
 Length 16;
 1; Indels
 Dove SG;
 84.3%; Score 70; DB 5; I
93.8%; Pred. No. 7.9e-06;
 Mason J,
 N-terminal amino acid sequence of a CFM #8.
 Mismatches
 Brugliera F,
 colour-facilitating molecule (CFM)
 Claim 4; Page 280; 510pp; English.
 ABB99068 standard; peptide; 16 AA.
 .
0
 Prescott M;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928.
 1 SVIAKQMTYKVYMSGT 16
 SVIAKOMTYKVNMSGT 16
 (first entry)
 Query Match
Best Local Similarity 93.8
Matches 15; Conservative
 QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 UV sink; sunscreen.
 (NUFA-) NUFARM LTD
 (JONE/) JONES E L.
 Sequence 16 AA;
 WO200270703-A2.
 UNIV
 22-JAN-2003
 white light.
 12-SEP-2002
 ABB99068;
 ABB99068
 RESULT
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0
expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruite and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light specira (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 flower industry; expression marker; reporter molecule; photon trap;
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent;
 .,
 Score 69; DB 5; Length 16; Pred. No. 1.2e-05; ly Mismatches 1; Indels
 Dove
 N-terminal amino acid sequence of a CFM #10.
 Mason J,
 1; Mismatches
 Brugliera F,
Prescott M;
 colour-facilitating molecule (CFM)
 Claim 4; Page 281; 510pp; English.
 ABB99070 standard; peptide; 16 AA.
 83.1%; 8
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 16
 01-MAR-2002; 2002WO-GB000928
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 (first entry)
 1 SVIAKOMTYKVYMSGT
 Query Match
Best Local Similarity 87.5
Matches 14; Conservative
 QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 Hoegh-Guldberg IO,
 UV sink; sunscreen
 (NUFA-) NUFARM LID
 (UYQU) UNIV QUEEN;
(JONE/) JONES E L.
 Sequence 16 AA;
 WO200270703-A2
 02-MAR-2001;
 Unidentified.
 22-JAN-2003
 12-SEP-2002.
 white light
 Jones EL,
 ABB99070:
 RESULT 6
 ABB99070
 888888888888
 à
 Db
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or include corolouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for

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0;
coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of mew varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein current sequence represents the N-terminal amino acid sequence of a colour-facilitating molecule (CFM)
 comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. Effes are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-white light.
 The invention relates to an isolated colour-facilitating molecule (CFM)
 Gaps
 Colour facilitating molecule, CFM; green fluorescent protein; GFP, chromophore, biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 ;
 83.1%; Score 69; DB 5; Length 16; 87.5%; Pred. No. 1.2e-05; ive 0; Mismatches 2; Indels
 Dove SG;
 Mason J,
 N-terminal amino acid sequence of a CFM #7.
 Brugliera F,
Prescott M;
 ABB99067 standard; peptide; 16 AA.
 Claim 4; Page 280; 510pp; English.
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 16
 01-MAR-2002; 2002WO-GB000928
 16
 (first entry)
 1 SVIAKOMTYKVYMSGT
 SVIVTOMTYKVYMSGT
 14; Conservative
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80.
 flower industry; ex
UV sink; sunscreen.
 Best Local Similarity
 (JONE/) JONES E
 Sequence 16 AA;
 WO200270703-A2.
 Unidentified
 22-JAN-2003
 12-SEP-2002
 ABB99067;
 Query Match
 Matches
 ABB99067
 RESULT 7
 g
 ò
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extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in chromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the NV-terminal amino acid sequence of a
 colour-facilitating molecule (CFM)
```

Sequence 16 AA;

```
;
0
 Gaps
 ;
Score 68; DB 5; Length 16;
Pred. No. 1.8e-05;
0; Mismatches 2; Indels
 0
 81.9%; 8
 14; Conservative
 Local Similarity
 Query Match
 Matches
 Best
```

16 SVIATOMIYKVYMPGT 16 1 SVIAKOMTYKVYMSGT

d d

ABB9907

ABB99071 standard; peptide; 16 AA. (first entry) 22-JAN-2003 

N-terminal amino acid sequence of a CFM #11.

Colour facilitating molecule; CFM; green fluorescent protein; GPP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; sink; sunscreen

Unidentified

WO200270703-A2.

12-SEP-2002.

01-MAR-2002; 2002WO-GB000928.

02-MAR-2001; 2001US-0273227P. 2001AU-00003874 15-OCT-2001; 2001US-0329816P 21-MAR-2001;

UNIV QUEENSLAND. (NUFA-) NUFARM LID JONES E L. (JONE/) UYQU )

Jones EL, Karan M, Hoegh-Guldberg IO,

WPI; 2002-740765/80.

Dove SG

Mason J,

Brugliera F,

Karan M,

Prescott M;

Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous nonwhite light

Claim 4; Page 281; 510pp; English.

The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous

The invention relates to an isolated colour-facilitating molecule (CFM)

```
cransgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of
 .
0
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 ÷
 80.7%; Score 67; DB 5; Length 16; 87.5%; Pred. No. 2.8e-05; rive 0; Mismatches 2; Indels
 Dove SG;
 Brugliera F, Mason J,
Prescott M;
 N-terminal amino acid sequence of a CFM #9.
 colour-facilitating molecule (CFM)
 ABB99069 standard; peptide; 16 AA.
 Claim 4; Page 280; 510pp; English.
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 1 SVIAKOMTYKVYMSGT 16
 01-MAR-2002; 2002WO-GB000928.
 1 SVSATOMTYKVYMSGT 16
 22-JAN-2003 (first entry)
 Query Match
Best Local Similarity 87.5'
Matches 14; Conservative
 NUFARM LTD.
UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80.
 UV sink; sunscreen
 Hoegh-Guldberg IO,
 (JONE/) JONES E L.
 Sequence 16 AA;
 WO200270703-A2.
 (NUFA-) NUFARM
 Unidentified
 12-SEP-2002.
 white light
 ABB99069;
 UYQU
 Jones
 RESULT 9
 ABB99069
 δ
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comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other cuses include transducing of intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for caring materials that experience UV damage e.g. plastics and car cupholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, corpusation markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their colours of distorted light spectra (biomatrix improve image quality in colours to be isolated was Green Fluorescent protein (GFP). The colour colour sequence represents the N-terminal amino acid sequence of a .. Gaps Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; · 0 79.5%; Score 66; DB 5; Length 16; 87.5%; Pred. No. 4.3e-05; rive 0; Mismatches 2; Indels /label= Xaa /note= "Xaa is any amino acid except Lys" /note= "Xaa is any amino acid except Met" note= "Xaa is any amino acid except Val" N-terminal amino acid sequence of a CFM #14. Location/Qualifiers colour-facilitating molecule (CFM) ABB99074 standard; peptide; 16 AA 21-MAR-2001; 2001AU-00003874. 15-OCT-2001; 2001US-0329816P. 01-MAR-2002; 2002WO-GB000928. 2001US-0273227P. 16 SGIATOMTYKVYMSGT 16 label= Xaa /label= Xaa (first entry) 1 SVIAKOMTYKVYMSGT Conservative (NUFA-) NUFARM LTD. (UYQU ) UNIV QUEENSLAND. (JONE/) JONES E L. sink; sunscreen. Query Match Best Local Similarity Matches 14; Conserv Misc-difference Misc-difference Misc-difference Sequence 16 AA; WO200270703-A2 02-MAR-2001; Unidentified 22-JAN-2003 L2-SEP-2002 ABB99074; (UYQU ) RESULT 10 ABB99074 g 

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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human ew in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel coloure e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs embedded in a gel matrix improve image quality in the flowering of distorted light species to enhance their marketability. CFMs embedded in a gel matrix improve image quality in chromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a
 ..
O
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule, CFM; green fluorescent protein, GFP, chromophore, biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 184.
 ..
 Score 62; DB 5; Length Lu, Pred. No. 0.00023;
 Length 16;
 Dove SG;
 Mason J,
 Brugliera F,
Prescott M;
 Claim 4; Page 282; 510pp; English.
 colour-facilitating molecule (CFM)
 ABP70008 standard; peptide; 13 AA.
 0,
 74.7%;
81.2%;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 16
 01-MAR-2002; 2002WO-GB000928
 (revised)
(first entry)
 1 SVIAKQMTYKVYMSGT
 1 SVIAKOMTYXXXXSGT
 Conservative
 Karan M,
 WPI; 2002-740765/80
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 Similarity
 UV sink; sunscreen
 Pavona decussata.
 Sequence 16 AA;
 WO200270703-A2.
 Mar
Local Simi
 06-AUG-2003
22-JAN-2003
 12-SEP-2002.
 white light
 ABP70008;
 Query Match
 Matches
 RESULT 11
 ABP70008
g
 THE SECOND SECON
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The invention relates to an isolated colour-facilitating molecule (CFW)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

cransgenic annual which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing coloured plant

catracts, e.g. flavouring, beverage or juice or colouring agent. Other

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

cating materials that experience UV damage e.g. plastics and car

conting materials that experience UV damage e.g. plastics and car

conting materials that experience UV damage e.g. plastics and car

conting materials that experience Other contemplated uses include,

conting materials plants. Other contemplated uses include,

conting markers, general reporter molecules, photon traps, UV sinks or

may manager so flowering plants. Other contemplated uses include,

charged species, and in fruits and vegetables to enhance their

marketability. CFMs embedded in a gel matrix improve image quality in

chromophore to be isolated was Green Fluorescent protein (GFP). The

sequences given in records ABB66924-ABP70048 represent CFM related amino

acid sequences given in records ABB6422-ABP7008 to correct OS field.)
 0
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Metalloprotease; enzyme; MP; p45; fusarium oxysporum; bacillus;
thermolysin; casein; Aspergillus oryzae.
 .;
0
 43.4%; Score 36; DB 5; Length 13; 100.0%; Pred. No. 10; cive 0; Mismatches 0; Indels
 Dove SG;
 Brugliera F, Mason J,
Prescott M;
 245 metalloprotease N-terminal fragment.
 AAR77526 standard; peptide; 14 AA.
 Claim 5; Page 473; 510pp; English
 95WO-US005534
 94US-00238108
 (first entry)
 8; Conservative
 QUEENSLAND.
 (revised)
 Karan M,
 SVIAKOMT 8
 WPI; 2002-740765/80
 Hoegh-Guldberg IO,
 Query Match
Best Local Similarity
 (NUFA-) NUFARM LTD
 Fusarium oxysporum
 (JONE/) JONES E L.
 SVIAKOMT
 Sequence 13 AA;
 3-MAY-1995;
 04-MAY-1994;
 25-MAR-2003
 12-JUN-1996
 16-NOV-1995
 Jones EL,
 AAR77526;
 Matches
 RESULT 12
```

```
0
 AAR77525-R77527 represent the N-terminal sequences of a fungal metalloprotease (MP). This sequence represents the N-terminus of Fusarium oxysporum MP P45 (see AAR77528). AAR77525 represents the consensus N-terminal sequence of the MP from F.oxysporum and Aspergillus oryzae. P45 is a new MP, and has 10 times more efficiency than Bacillus MP. Bacillus MP is more effective in cleaving primary amino groups from casein. P45 has thermolysin-like activity, and is used to cleave a pro-sequence from a recombinant proenzyme to generate an active mature enzyme. The MP may be added to, or produced in, the broth where the proenzyme is being formed by a recombinant host cell converted with a vector containing the DNA encoding P45. The MP can also be used to assay the level of activity activity and is used to assay the level of activity activitable proenzyme in a sample. (Updated on 25-MAR-2003 to correct PA
 Fungal metallo:protease converts pro:enzyme to active form - has thermolysin-like activity, useful to cleave pro-sequence of pro:enzyme to
 Gaps
 Host cell with reduced expression of metallo-protease - for prodn. of
 0
 Metalloprotease; protease; p45; recombinant protein; host cell.
 ŝ
 Fusarium oxysporum p45 metalloprotease N-terminal peptide.
 Length 14;
 34.9%; Score 29; DB 2; Length 14; 75.0%; Pred. No. 2.2e+02; tive 0; Mismatches 2; Indels
 Branner
 Fuglsang C,
 recombinant proteins, opt. as their precursors
 Fusarium oxysporum; strain DSM 2672.
 AAW05846 standard; peptide; 14 AA.
 Madden M,
 Claim 12; Page 36; 62pp; English.
 Example 1; Page 34; 51pp; English
 (NOVO) NOVO NORDISK BIOTECH INC. (NOVO) NOVO-NORDISK AS.
95US-00398489.
 96WO-DK000111.
 (first entry)
 Query Match
Best Local Similarity 75.v.
6; Conservative
 (NOVO) NOVO-NORDISK AS
 generate mature enzyme.
 (revised)
 8 TYKVYMSG 15
 WPI; 1996-443168/44.
 WPI; 1995-404122/51.
 σ
 2 TYKVYPWG
 Sequence 14 AA;
03-MAR-1995;
 20-MAR-1996;
 WO9629391-A1
 20-MAR-1995;
 16-OCT-2003
28-JAN-1997
 26-SEP-1996
 Lehmbeck J;
 AAW05846;
 field.)
 RESULT 13
 AAW05846
 AC SECOND à
 g
```

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T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatablilty complex; MHC; B cell; disease; anti-tumour; anti-viral.
 Human melanoma associated protein tyrosinase peptide (pos. 367-377).
 Method of selecting T cell peptide epitope(s) - by measuring the stability of HLA class I-peptide complexes on intact B cells.
 AAW39598 standard; peptide; 11 AA.
 Van Der Burg SH, Kast WM,
 (UYLE-) RIJKSUNIV LEIDEN
 WPI; 1997-549891/50.
 Homo sapiens.
 WO9741440-A1.
 28-APR-1997;
 26-APR-1996;
 11-JUN-1998
 23-DEC-1996;
 06-NOV-1997.
 (SCIS-)
AAW39598
 ò
 q
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0
 metalloprotease (see also AAWOS845) was identified by amino acid analysis of a protein isolated from a fermentation broth. A PCR primer based on this peptide was used, together with a primer based on a p45 internal peptide, in the PCR cloning of the p45 gene (AAT40133) from F. oxysporum genomic DNA. (Updated on 16-OCT-2003 to standardise OS field)
 The present invention provides the protein and coding sequences of human zinc finger protein 53. The sequences can be used in the treatment of cancer, haemopathy, nervous system disorders, development disorders, metabolic disorders, inflammation, immunological diseases and HIV inflection. The present sequence is the N-terminus of the protein of the
 The N-terminal sequence (AAW05846) of Fusarium oxysporum DSM 2672 p45
 Gaps
 polypeptide-human zinc finger protein 53 and polynucleotide for
 Human, zinc finger protein 53; cancer; nervous system disease; development disorder; metabolic disease; inflammation; haemopathy; immunological disease; HIV infection; gene therapy.
 0
 34.9%; Score 29; DB 5; Length 15; 54.5%; Pred. No. 2.3e+02; ive 1; Mismatches 4; Indels
 Length 14;
 Score 29; DB 2; Length 14;
Pred. No. 2.2e+02;
0; Mismatches 2; Indels
 Human zinc finger protein 53 N-terminal peptide.
 Example 6; Page 18(Disclosure); 33pp; Chinese.
 (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 AAM48968 standard; peptide; 15 AA.
 0
 17-MAR-2000; 2000CN-00114979.
 17-MAR-2000; 2000CN-00114979
 Query Match 34.9%;
Best Local Similarity 75.0%;
Matches 6; Conservative
 (first entry)
 coding such polypeptide
 WPI; 2002-056224/08.
 8 TYKVYMSG 15
 σ
 TYKVYPWG
 Sequence 15 AA;
 Sequence 14 AA;
 Homo sapiens.
 25-APR-2002
 CN1314368-A.
 01
 AAM48968;
 Query Match
 Mao Y,
 AAM48968
ID AAM4
```

Melief CJM;

Toes REM, Offringa R,

SCI SEED CAPITAL INVESTMENTS BV.

97WO-NL000229. 96EP-00201145 96EP-00203670

g

(first entry)

```
ö
 Peptides AAW39430 W39734 are used in a novel method for the selection of immunogenic T-cell peptide epitopes present in polypeptide antigens. The method involves the identification of peptide sequences capable of binding to an HLA (human leukocyte antigen) class I molecule and measuring the binding of this epitope peptide to the HLA class I peptide. The stability of binding of the peptide and MHC (major histocompatability complex) class I molecule is measured on intact human B cells carrying the MHC molecule at their cell surfaces. The method can be used to select peptide epitopes for generating vaccines against a disease associated with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral immune responses. Peptide AAW39598 is derived from the human melanoma associated protein tyrosinase which is capable of upregulating HLA-A*0201
 Gaps
 ..
 Length 11;
 0; Indels
 Score 28; DB 2; I
Pred. No. 2.5e+02;
3; Mismatches 0;
 Search completed: August 12, 2004, 07:03:22
Example 3; Page 75; 109pp; English.
 33.7%;
57.1%;
 Ouery Match
Best Local Similarity 5/...
4, Conservative
 11 VYMSGTV 17
 Sequence 11 AA;
 Job time : 51 secs
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Gaps

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Conservative 5 KOMTYKVYMSG 15

Best\_Local Similarity Matches 6; Conserv

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KNMTLKSFASG 12

RESULT 15

us-09-890-463-4.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2004, 06:12:47; Search time 89.0881 Seconds (without alignments) 745.314 Million cell updates/sec Run on:

US-09-890-463-4 1287 Title:

1 SVIAKQMTYKVYMSGTVNGH......KPVVACRFFRVKSRHKYAVA 235 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2011s:\*
geneseqp2012s:\*
geneseqp2013bs:\*
geneseqp2013bs:\* A\_Geneseq\_29Jan04:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTES

|               |       | ж              |        |    | SUMMAKIES |                    |
|---------------|-------|----------------|--------|----|-----------|--------------------|
| Result<br>No. | Score | Query<br>Match | Length | DB | ID        | Description        |
|               | 1287  | 100.0          | 235    |    | ¥9        | Aay97150 Pigment p |
| 7             | 1279  | 99.4           | 235    | Ŋ  | ABP70042  | Colour F           |
| m             | 1257  | 7.76           | 235    | Ŋ  | ABP70026  |                    |
| 4             | 1242  | 96.5           | 231    | m  | AAY97149  | Aay97149 Pigment p |
| Ŋ             | 1242  | 96.5           | 231    | Ŋ  | ABP70025  | Colour F           |
| φ             | 1190  | 92.5           | 226    | Ŋ  | ABP70036  |                    |
| 7             | 1188  | 92.3           | 220    | ហ  | ABP70037  | Abp70037 Colour Fa |
| 00            | 1174  | 91.2           | 220    | Ŋ  | ABP69926  | Abp69926 Colour Fa |
| 9             | 1174  | 91.2           | 223    | ഗ  | ABP70030  | Abp70030 Colour Fa |
| 10            | 1174  | 91.2           | 223    | Ŋ  | ABP70032  | Abp70032 Colour Fa |
| 11            | 1169  | 8.06           | 221    | Ŋ  | ABP69992  | Abp69992 Colour Fa |
| 12            | 1169  | 8.06           | 221    | 5  | ABP69991  | -                  |
| 13            | 1166  | 90.6           | 220    | Ŋ  | ABP70007  |                    |
| 14            | 1165  | 90.5           | 221    | Ŋ  | ABP69967  | Abp69967 Colour Fa |
| 15            | 1165  | 90.5           | 221    | Ŋ  | ABP69966  | Abp69966 Colour Fa |
| 16            | 1165  | 90.5           | 221    | Ŋ  | ABP70004  | Abp70004 Colour Fa |
| 17            | 1165  | 90.5           | 223    | Ŋ  | ABP70033  | _                  |
| 18            | 1165  | 90.5           | 235    | 2  | ABP69963  | ~                  |
| 19            | 1165  | 90.5           | 235    | 2  | ABP69961  | Abp69961 Colour Fa |
| 20            | 1164  | σ              | 221    | 2  | ABP69978  | Abp69978 Colour Fa |
| 21            | 1163  | σ              | 223    | 2  | ABP70029  | Abp70029 Colour Fa |
| 22            | 1162  | σ              | 220    | 2  | ABP69941  | Abp69941 Colour Fa |
| 23            | 1162  | 90.3           | 220    | 2  | ABP69940  | _                  |
| 24            |       | 90.2           | 220    | S  | ABP69952  | Abp69952 Colour Fa |
| 25            | 1161  | 90.2           | 220    | 2  | ABP69959  | Abp69959 Colour Fa |

| Fа       | FЗ       | Fа       | Fa       | Fa       | Ēά       | Fа       | ъ        | Fa       | Fa       | Fa       | Fa       | Fа       | Fa       | Fa       | Fа       | Fа       | E<br>E   | н<br>Б   | Fа       |
|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| Colour   | Colour   | Colour   | Colour   | -        |          | Colour   |          |          | Colour   | Colour   | _        |          | Colour   |
| Abp69934 | Abp69958 | Abp69937 | Abp69935 | Abp69972 | Abp70027 | Abp69939 | Abp69965 | Abp70002 | Abp69938 | Abp70031 | Abp69925 | Abp69964 | Abp69993 | Abp69989 | Abp69986 | Abp69930 | Abp69999 | Abp70035 | Abp69936 |
|          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |          |
| 5993     | ABP69958 | ABP69937 | ABP69935 | ABP69972 | ABP70027 | ABP69939 | ABP69965 | ABP70002 | ABP69938 | ABP70031 | ABP69925 | ABP69964 | ABP69993 | ABP69989 | ABP69986 | ABP69930 | ABP69999 | ABP70035 | ABP69936 |
| 2        | Ŋ        | Ŋ        | Ŋ        | ις.      | Ŋ        | Ŋ        | Ŋ        | Ŋ        | Ŋ        | r        | Ŋ        | Ŋ        | Ŋ        | ហ        | Ŋ        | ហ        | Ŋ        | Ŋ        | 2        |
| 220      | 220      | 220      | 220      | 221      | 222      | 220      | 220      | 221      | 220      | 223      | 220      | 220      | 220      | 220      | 221      | 220      | 220      | 221      | 220      |
| 90.2     | 90.2     | 90.2     | 90.2     | 90.2     |          | 90.1     | 0.06     | 0.06     | 89.9     |          |          | 89.8     | 89.7     | 89.7     | 89.7     | 89.7     | 89.5     | 89.5     | 89.4     |
| 1161     | 1161     | 1161     | 1161     | 1161     | 1159.5   | 1159     | 1158     | 1158     | 1157     | 1157     | 1156     | 1156     | 1155     | 1155     | 1155     | 1154     | 1152     | 1152     | 1151     |
|          |          |          | 29       | 30       | 31       | 32       | 33       | 34       | 35       | 36       | 37       | 38       | 39       | 40       | 41       | 42       | 43       | 44       | 45       |

#### ALIGNMENTS

```
Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 N-terminal; pigment protein from coral tissue; PPCT; fluorescence; tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet; UV filter; POC3.
 the
 the
 'note= "critical residue in the vicinity of the
 /note= "critical residue in the vicinity of
 /note= "critical residue in the vicinity of
 /label= Chromophore_motif
 Pigment protein from coral tissue POC4.
 Location/Qualifiers
 AAY97150 standard; protein; 235 AA.
 02-FEB-2000; 2000WO-AU000056.
 fluorophore"
 fluorophore"
 fluorophore"
 ŝ
 (first entry)
 Hoegh-Guldberg O, Dove
 WPI; 2000-532892/48.
N-PSDB; AAA52083.
 (UNSY) UNIV SYDNEY.
 Misc-difference 158
 Misc-difference 192
 Misc-difference 210
 Misc-difference 61
 Acropora aspera.
 WO200046233-A1
 02-FEB-1999;
 04-DEC-2000
 10-AUG-2000
 AAY97150;
RESULT 1
 AAY97150
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 OYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKAKK 180
 light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dysetuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters (both
 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 60
 1 SVIAKOMIYKVYMSGIVNGHYFEVEGDGKGKPYEGEQTVRLAVIKGGPLPFAWDILSPQC 60
 cDNA libraries were constructed from a blue pigmented coral, Acropora aspera to isolate sequences encoding polypeptides with N-terminal sequences as shown in AAV9147-48. Pigment protein from coral tissue (PPCT) is capable of emitting fluorescence upon irradiation by incident
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVACRFFRVKSRHKYAVA 235
 PVKMPGYHYVDRKLDVTNHNKDYISVEQCEISIARKPVVACRFFRVKSRHKYAVA 235
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Novel color-facilitating molecule for producing a biomatrix, has a
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 245.
 100.0%; Score 1287; DB 3; Length 235; 100.0%; Pred. No. 1.2e-127; ive 0; Mismatches 0; Indels 0.
 SG;
 Dove
 Mason J,
 Claim 13; Page 43-44; 49pp; English.
 ABP70042 standard; protein; 235 AA
 Brugliera F,
Prescott M;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 (first entry)
 Conservative
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80
 Best Local Similarity
Matches 235; Conserv
 sink; sunscreen
 JONES E L.
 Sequence 235 AA;
 Acropora aspera
 WO200270703-A2.
 22-JAN-2003
 12-SEP-2002.
 ABP70042;
 121
 121
 181
 Query Match
 (UYQU)
(JONE/)
 RESULT 2
ABP70042
THE STATE OF THE S
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include.
 180
 expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra light spectra all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 120
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 9
 9
polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILLSPQC
 QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 SVIAKOMIYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 Gaps
 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVACRFFRVKSRHKYAVA 235
 PVKMPGYHYVDRKLDVTNHNKDYTSVEOCELSIARKPVVACRFFRVKSRHKVAVA 235
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 202
 .,
 Length 235;
 1; Indels
 Score 1279; DB 5;
Pred. No. 8.7e-127;
0; Mismatches 1;
 Example 20; Page 502-503; 510pp; English.
 ABP70026 standard; protein; 235
 99.4%;
 (first entry)
 Conservative
 (revised)
 Query Match
Best Local Similarity
Matches 234; Conserv
 sink; sunscreen.
 Sequence 235 AA;
 WO200270703-A2
 acid sequences
 Unidentified
 white light.
 12-SEP-2002.
 06-AUG-2003
22-JAN-2003
 ABP70026;
 61
 181
 flower
UV sink
 ABP70026
 RESULT
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04-DEC-2000 (first entry)

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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or manneral fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in thromotore to be isolated to be accounted.
 chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.)
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Brugliera F, Mason J, Prescott M;
 Claim 5; Page 479; 510pp; English.
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
01-MAR-2002; 2002WO-GB000928
 15-OCT-2001; 2001US-0329816P
 UNIV QUEENSLAND.
JONES E L.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80
 NUFARM LID
 white light
 (UYQU)
(JONE/)
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SG; Dove

Best Local Similarity Sequence 235 AA; Query Match Matches

0 QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKRS 120 GLINFPPNGPVMQKKTQGWEPNTERLFARDGML1GNNFMALKLEGGGHYLCEFKSTYKAKK 180 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGLPYEGGQTVRLAVTKGGPLPFAWDILSPQC 60 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 60 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKAKK Gaps PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVACRFFRVKSRHKYAVA 235 . 0 Length 235; 4; Indels 97.7%; Score 1257; DB 5; 98.3%; Pred. No. 1.9e-124; iive 0; Mismatches 4; 231; Conservative 19 61 121 121 181 181 g à ò ð δ

AAY97149 standard; protein; 231 AA.

RESULT 4 AAY97149 AAY97149

RXXX

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120
 120
 GINFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 cDNA libraries were constructed from a blue pigmented coral, Acropora aspera to isolate sequences encoding polypeptides with N-terminal sequences as shown in AAY97147-48 bigment protein from coral tissue (PPCT) is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dysetuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters (both
 9
 09
 Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 N-terminal; pigment protein from coral tissue; PPCT; fluorescence;
tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet;
 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 Gaps
 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 'note= "critical residue in the vicinity of the
 'note= "critical residue in the vicinity of the
 0;
 96.5%; Score 1242; DB 3; Length 231;
 'note= "critical residue in the vicinity of
 2; Indels
 Pred. No. 7e-123;
2; Mismatches
 51. .63
/label= Chromophore_motif
 Pigment protein from coral tissue POC3
 Claim 13; Page 42-43; 49pp; English.
 Location/Qualifiers
 fluorophore"
 02-FEB-2000; 2000WO-AU000056
 fluorophore"
 99AU-00008463
 98.3%;
 fluorophore
 Hoegh-Guldberg O, Dove S;
 Matches 227; Conservative
 2000-532892/48.
 (UNSY) UNIV SYDNEY.
 Misc-difference 192
 Misc-difference 210
 Misc-difference 158
 Best Local Similarity
 Misc-difference 61
 UV filter; POC3.
 N-PSDB; AAA52082
 Sequence 231 AA;
 Acropora aspera
 WO200046233-A1
 02-FEB-1999;
 10-AUG-2000
 Query Match
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DB 5; Length 231;

Score 1242;

Query Match

g δ

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Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVACRFFRVKSRHK 231
 PUKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRHK 231
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 201.
 SG;
 Dove
 Mason J,
 ABP70025 standard; protein; 231 AA
 Brugliera F,
Prescott M;
 6; Page 478; 510pp; English.
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 (revised)
(first entry)
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
(JONE/) JONES E L.
 Karan M,
 WPI; 2002-740765/80
 sink; sunscreen
 Hoegh-Guldberg IO,
 WO200270703-A2
 Jnidentified.
 22-JAN-2003
 12-SEP-2002.
 06-AUG-2003
 white light
 ABP70025;
181
 181
 Claim
 Jones
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The invention relates to an isolated colour-facilitating molecule (CFW) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other ess include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Pluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.)

Sequence 231 AA;

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 The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other
 120
 180
 120
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGGHYLCEFKSTYKARK 180
 9
 09
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 61 QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
 1 SVIAKQMTYKVYMSGTVNGHYFBVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVACRFFRVKSRHK 231
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRHK 231
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 238
 .,
 Indels
 SG;
 Dove
 5
 Pred. No. 7e-123;
2; Mismatches
 Mason J,
 Example 19; Page 496-497; 510pp; English.
 Š
 Brugliera F,
Prescott M;
 ABP70036 standard; protein; 226
96.5%;
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 02-MAR-2001; 2001US-0273227P
 (revised)
(first entry)
 Best Local Similarity 98.3
Matches 227; Conservative
 QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 UV sink; sunscreen
 (NUFA-) NUFARM LTD
 (UYQU) UNIV QUE
(JONE/) JONES E
 WO200270703-A2.
 22-JAN-2003
 12-SEP-2002
 white light
 06-AUG-2003
 ABP70036;
 61
 RESULT 6
 ABP70036
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uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for cotaing materials that experience VV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.) 

Sequence 226 AA;

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ö
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 61 QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 SVIAKOMIYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS 60
 1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 60
 Gaps
 .
0
92.5%; Score 1190; DB 5; Length 226; 96.9%; Pred. No. 2.2e-117; ive 1; Mismatches 6; Indels C
 PVRMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVAMCFFRV 226
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVACRFFRV 226
 Local Similarity 96.9
nes 219; Conservative
 61
 181
 181
 Query Match
 Matches
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Colour Facilitating molecule (CFM) related sequence #SEQ ID 239. ABP70037 standard; protein; 220 AA (revised)
(first entry) 06-AUG-2003 22-JAN-2003 ABP70037; RESULT 7 ABP70037 

Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen

WO200270703-A2

01-MAR-2002; 2002WO-GB000928. 12-SEP-2002.

2001US-0273227P. 21-MAR-2001; 2001AU-00003874 15-OCT-2001; 2001US-0329816P 02-MAR-2001; 21-MAR-2001;

QUEENSLAND. (NUFA-) NUFARM LTD (UYQU ) UNIV QUEEN (JONE/) JONES E L. Mason J, Brugliera F, Prescott M; Karan M, Hoegh-Guldberg IO, Jones EL,

Dove SG;

WPI; 2002-740765/80

The invention relates to an isolated colour-facilitating molecule (CFW) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing photorropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upolstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, cypression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their 120 situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP6924-ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.) 09 09 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 1 SVIAKOMIYKVYMSGIVNGHYFEVEGDGKGKPYEGEQIVRLAVIKGGPLPFAWDILSPQC marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-prote Gaps ·. 1; Indels 92.3%; Score 1188; DB 5; 98.6%; Pred. No. 3.4e-117; 2; Mismatches Example 19; Page 497-498; 510pp; English. Matches 217; Conservative Query Match Best Local Similarity Sequence 220 AA; white light

QYGSIPPTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS g a 8

GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA 220 셤 ð ð

180

g

ABP69926 standard; protein; 220 RESULT 8 ABP69926

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(first entry) 22-JAN-2003 

ABP69926;

Colour Facilitating molecule (CFM) related sequence #SEQ ID 24

Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; flower industry; ex UV sink; sunscreen.

WO200270703-A2.

12-SEP-2002

01-MAR-2002; 2002WO-GB000928

Colour Facilitating molecule (CFM) related sequence #SEQ ID 216.

(first entry)

22-JAN-2003

Dove SG;

Мавоп Ј,

The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules; imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a carracteristic sheep with blue or red coloured fleece. They are useful for producing coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other cases include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plantics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs embedded in a gel matrix improve image quality in alturations of distorted light specira (blomatrix). The first all-protein contemplated in a gel matrix improve image quality in a colour or the colour in the situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-ABP70030 standard; protein; 223 AA. Brugliera F, Prescott M; Claim 5; Page 289; 510pp; English. 2001US-0273227P 21-MAR-2001; 2001AU-00003874 15-OCT-2001; 2001US-0329816P 215; Conservative (UYQU ) UNIV QUEENSLAND. Jones EL, Karan M, Hoegh-Guldberg IO, WPI; 2002-740765/80 (NUFA-) NUFARM LTD (UYOU ) UNIV QUEEN! Query Match Best Local Similarity Sequence 220 AA; 02-MAR-2001; white light - 19 ABP70030; 121 121 181 181 Matches ABP70030
ID ABP7
XX
AC ABP7 RESULT 9 g ð  $\delta$ Db ð

ö QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFWALKLEGGGGHYLCEFKSTYKAKK 180 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS 60 QYGSIPFTKXPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC Gaps ., 5; Length 220; 4; Indels PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA 220 PVRMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA 220 91.2%; Score 1174; DB 5; 97.7%; Pred. No. 1e-115; iive 1; Mismatches 4

120

9 61 SVIAKQMIYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPPAMDILSPQS QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS

N 61 62

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1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC

The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured flaece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of heavened and plants. Other contemplated uses include, sinks or expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CPMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CPMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GPP). The sequences given in records ABP69924-ABP70048 represent CPM related amino Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-Gaps Colour facilitating molecule, CFM; green fluorescent protein, GFP; chromophore, biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; ., Length 223; Indels Dove SG; DB 5; 91.2%; Score 1174; DB 5; 97.7%; Pred. No. 1.1e-115; Mason J, 1; Mismatches Example 18; Page 486; 510pp; English. Brugliera F, Prescott M; 02-MAR-2001; 2001US-0273227P. 21-MAR-2001; 2001AU-00003874. 15-OCT-2001; 2001US-0329816P. 01-MAR-2002; 2002WO-GB000928 Best Local Similarity 97.7 Matches 215; Conservative NUFARM LTD. UNIV QUEENSLAND. Karan M, WPI; 2002-740765/80 flower industry; ex UV sink; sunscreen. Jones EL, Karan M, Hoegh-Guldberg IO, Sequence 223 AA; (UYQU ) UNIV QUE (JONE/) JONES E WO200270703-A2 Tubastrea sp 12-SEP-2002 Query Match (NUFA-) white 

us-09-890-463-4.rag

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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algea and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include.
GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGGHYLCEFKSTYKAKK 180
 GINFPPNGPVMQKKTQGWEDNTERLFARDGWLIGNNFWALKLEGGGHYLCEFKSTYKAKK 181
 polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Novel color-facilitating molecule for producing a biomatrix, has a
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 220.
 SG;
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA 221
 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA
 Dove
 Mason J,
 Disclosure; Page 489; 510pp; English.
 ABP70032 standard; protein; 223 AA
 Brugliera F,
Prescott M;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 (first entry)
 QUEENSLAND.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80
 flower industry; ex. UV sink; sunscreen.
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENE
 JONES E L.
 WO200270703-A2.
 Sinularia sp.
 22-JAN-2003
 12-SEP-2002,
 white light
121
 122
 ABP70032;
 (UYQU)
(JONE/)
 RESULT 10
ABP70032
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expression markers, general reporter molecules, photon traps, UV sinks or in unscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (FPP). The sequences given in records ABP69924-ABP700048 represent CFM related amino

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ó
 120
 121
 121 GLNFPPNGFVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 GINFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKAKK 181
 The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or trogether with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous
 09
 61
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 2 SVIAKQMIYKVIMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVIKGGPLPFAWDILSPQC
 61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 62 QYGSIPFIKYLEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 Gaps
 chromophore, biomatrix, transgenic animal, colouring agent,
flower industry, expression marker, reporter molecule, photon trap,
 Colour facilitating molecule; CFM; green fluorescent protein; GFP;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 149.
 .
0
 Length 223;
 Indels
 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA 220
 182 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPLVA 221
 Dove SG;
 3
 Score 1174; DB 5;
Pred. No. 1.1e-115;
 Mason J,
 2; Mismatches
 Claim 6; Page 435-436; 510pp; English.
 Z
 Brugliera F,
 ABP69992 standard; protein; 221
 Prescott M;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 91.2%;
 01-MAR-2002; 2002WO-GB000928
 (revised)
(first entry)
 Conservative
 UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 Query Match
Best Local Similarity
 flower industry; ex
UV sink; sunscreen.
 Hoegh-Guldberg IO,
 (NUFA-) NUFARM LTD
 (JONE/) JONES E L.
 Sequence 223 AA;
 Pocillopora sp.
 WO200270703-A2.
acid sequences
 06-AUG-2003
22-JAN-2003
 12-SEP-2002
 white light
 Matches 215;
 122
 ABP69992;
 Jones EL
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 RESULT 11
 ABP69992
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transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured fleece. They are useful for producing coloured plant catactories, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plaatics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in chromophore to be isolated was Green Fluorescent protein (GFP). The chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP66924 ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.)
 ò
 120
 121
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFWALKLEGGGGHYLCEFKSTYKAKK 180
 181
 09
 61
 GLNFPPNGPVMQXKTQGWEPHSERLFARDGMLIGNNFWALKLEGGGHYLCEFKTTYKAKK
 1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 2 SVIATQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPPAWDILSPQC
 61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 147.
 0;
 Length 221;
 emission. CFMs are useful for
 3; Indels
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA 220
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA 221
 Score 1169; DB 5;
Pred. No. 3.6e-115;
4; Mismatches 3;
 ABP69991 standard; protein; 221 AA
 90.8%;
96.8%;
 02-MAR-2001; 2001US-0273227P
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
non-white light or particle
 (first entry)
 Matches 213; Conservative
 NUFARM LTD.
UNIV QUEENSLAND.
JONES E L.
 (revised)
 Local Similarity
 sink; sunscreen
 Sequence 221 AA;
 Pocillopora sp.
 WO200270703-AZ.
 22-JAN-2003
 L2-SEP-2002.
 06-AUG-2003
 ABP69991;
 181
 Query Match
 62
 121
 122
 (UYQU)
 (NUFA-)
 RESULT 12
 ABP69991
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The invention relates to an isolated colour-facilitating molecule (CFW) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a cransgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant or ted soloured fleece. They are useful for producing agent. Other east sinclude transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car conting materials that experience UV damage e.g. plastics and car conting markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs embedded in a qel matrix improve image quality in charactions of distorted light species to enhance their and vegetables to enhance their anticons of distorted light specira (Diomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABBF09924-ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.)
 180
 61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 121
 122 GLNFPPNGPVMQKKTQGWEPHSERLFARDGMLIGNNFMALKLEGGGHYLCEFKTTYKAKK 181
 09
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 61
 62 QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 2 SVIATOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 177.
 .
0
 Length 221;
 Dove SG;
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA 221
 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA
 90.8%; Score 1169; DB 5;
96.8%; Pred. No. 3.6e-115;
ive 4; Mismatches 3;
 Mason J,
 Claim 6; Page 433-434; 510pp; English.
 Œ,
 4;
 ABP70007 standard; protein; 220
Brugliera :
 (first entry)
 Best Local Similarity 96.8 Matches 213; Conservative
Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80
 flower industry; ex
UV sink; sunscreen.
 Sequence 221 AA;
 Montipora sp
 22-JAN-2003
 white light
 ABP70007;
 Query Match
 RESULT 13
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The invention relates to an isolated colour-facilitating molecule (CFW) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or erd coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include,
 expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CPMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CPMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GPP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Mason J,
 Claim 6; Page 467-468; 510pp; English.
 Brugliera F,
 Prescott M;
 02-MAR-2001; 2001US-0273227P.
 01-MAR-2002; 2002WO-GB000928
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 (UYQU) UNIV QUEENSLAND. (JONE/) JONES E L.
 Karan M,
 WPI; 2002-740765/80.
 (NUFA-) NUFARM LTD.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WO200270703-A2.
 acid sequences
 12-SEP-2002
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Dove SG;

Sequence 220 AA;

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o;
 120
 QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 121 GENFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 9
 1 SVIVTQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQY 60
 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 Gaps
 .
0
 Length 220;
 Indels
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA 220
 90.6%; Score 1166; DB 5;
97.3%; Pred. No. 7.4e-115;
ive 0; Mismatches 6;
 9
 Conservative
Query Match
Best Local Similarity
Matches 214; Conserv
 181
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 61
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The invention relates to an isolated colour-facilitating molecule (CFM)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

non-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

ced coloured fleece. They are useful for producing coloured plant

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

uses include transducing or intensifying an image, providing additional

light for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

cupholstery. CFMs are useful in the flower industry, in the development of

men varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs modify visible colour in edible and/or ornamental

fungal species, and in fruits and vegetables to enhance their

chromophore to be isolated was Green Fluorescent protein (GFP). The

chromophore to be isolated was Green Fluorescent protein (GFP). The

contemplate or the process given in records Ampergoat American CFM related amino Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; Colour Facilitating molecule (CFM) related sequence #SEQ ID 102. acid sequences. (Updated on 06-AUG-2003 to correct OS field.) 90.5%; Score 1165; DB 5; Length 221; 96.4%; Pred. No. 9.5e-115; Live 4; Mismatches 4; Indels ( Dove SG; Brugliera F, Mason J, Prescott M; Claim 5; Page 383-384; 510pp; English. ABP69967 standard; protein; 221 AA. 02-MAR-2001; 2001US-0273227P. 21-MAR-2001; 2001AU-00003874. 15-OCT-2001; 2001US-0329816P. 01-MAR-2002; 2002WO-GB000928. (first entry) Query Match 90.5 Best Local Similarity 96.4 Matches 212; Conservative (NUFA-) NUFARM LID. (UYQU ) UNIV QUEENSLAND. (JONE/) JONES E L. (revised) Jones EL, Karan M, Hoegh-Guldberg IO, WPI; 2002-740765/80. UV sink; sunscreen Acropora aspera. Sequence 221 AA; WO200270703-A2. 06-AUG-2003 22-JAN-2003 12-SEP-2002. white light. ABP69967; ABP69967 

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RESULT 14

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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for cating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
SVIATQMTYKVYMSGTVNGHYFEVEGBGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 61
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 QYGSIPFTKYPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 100.
 220
 PVKMPGYHYVDRKLDVTNHNKDYTSVEOCEISITRKPVVA 221
 Dove SG;
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA
 Mason J,
 Claim 5; Page 381-382; 510pp; English.
 ABP69966 standard; protein; 221 AA
 Brugliera F,
Prescott M;
 02-MAR-2001; 2001US-0273227P.
 01-MAR-2002; 2002WO-GB000928.
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 (first entry)
 QUEENSLAND.
 (revised)
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80.
 flower industry; ex
UV sink; sunscreen
 (NUFA-) NUFARM LTD
 Acropora aspera.
 WO200270703-A2
 (JONE/) JONES
 06-AUG-2003
 22-JAN-2003
 12-SEP-2002.
 ABP69966;
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0
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 QYGSIPFIKXPEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 121
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.)
 9
 61
 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 2 SVIATOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
modify visible colour in edible and/or ornamental
 Gaps
 ..
0
 Length 221;
 Indels
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA 220
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISITRKPVVA 221
 4.
 90.5%; Score 1165; DB 5; 96.4%; Pred. No. 9.5e-115; iive 4; Mismatches 4;
 Matches 212; Conservative
 in sunscreens. CFMs
 Query Match
Best Local Similarity
 Sequence 221 AA;
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Search completed: August 12, 2004, 06:17:06 Job time : 90.0881 secs

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August 12, 2004, 06:12:47; Search time 61.1578 Seconds (without alignments) 1212.385 Million cell updates/sec
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1287
1 SVIAKQMTYKVYMSGTVNGH......KPVVACRFFRVKSRHKXAVA 235
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1017041 seqs, 315518202 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 sp_plant:*
sp_rodent:*
sp_virus:*
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Gapop 10.0 , Gapext 0.5
 1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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5: sp_invertebrate:*
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 Minimum DB seq length: 0
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 Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |   |        | Description     | Q95p04 goniopora t | Q9u6y8 discosoma s | Q9qtj7 discosoma s | -      | Q8t6u0 dendronepht | Q963f5 montastraea | Q7z0w4 montastraea |        | Q9u6y3 clavularia | Q7z0w6 montastraea | Q7z0w9 montastraea | Q962p9 montastraea |        | Q95ua7 montastraea | Q8t5f1 montastraea | Q95vt0 montastraea |
|-----------|---|--------|-----------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------|-------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|
| SUMMARIES |   |        | QI .            | Q95P04             | 8X9n6ŏ             | Q9GTJ7             | Q9U6Y7 | QBIGUO             | Q963F5             | Q7Z0W4             | Q7Z0W5 | Q9U6Y3            | Q7Z0W6             | 07Z0W9             | Q962P9             | Q7Z0W8 | Q95UA7             | QBT5F1             | Q95VT0             |
|           |   |        | BB              | 5                  | Ŋ                  | S                  | 2      | 2                  | Ŋ                  | Ŋ                  | Ŋ      | ហ                 | 'n                 | w                  | Ŋ                  | 'n     | n                  | S                  | Ŋ                  |
|           |   |        | Match Length DB | 221                | 225                | 230                | 232    | 236                | 225                | 225                | 225    | 266               | 227                | 225                | 227                | 227    | 225                | 225                | 227                |
|           | % | Query  | Match           | 89.8               | 60.8               | 58.3               | 57.3   | 54.9               | 54.9               | 54.5               | 52.4   | 52.1              | 52.0               | 51.9               | 51.9               | 51.9   | 51.8               | 51.0               | 50.9               |
|           |   |        | Score           | 1156               | 783                | 750                | 737.5  | 707                | 706                | 701                | 674    | 671               | 669.5              | 667.5              | 667.5              | 667.5  | 666.5              | 656.5              | 654.5              |
|           |   | Result | No.             | М                  | 73                 | Э                  | 4      | ហ                  | φ                  | 7                  | 89     | <u>ο</u>          | 10                 | 11                 | 12                 | 13     | 14                 | 15                 | 16                 |

|                                  |                                       | Valsis parabicyoni<br>QBmmal agaricia ag<br>QBmu46 ricordea fl<br>Q9gpi5 anemonia su<br>Q95w86 condylactis<br>Q95w85 radianthus | Q95w11 condylactis Q9gz28 anemonia su Q9gpi6 anemonia su Q8mu45 condylactis Q8t5f0 scolymia cu Q8c17 meandrina m                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                          |
|----------------------------------|---------------------------------------|---------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------|
|                                  |                                       | 5 Q8MA1<br>5 Q8MA1<br>5 Q9GDI5<br>5 Q9GN86<br>5 Q95W86                                                                          | 5 Q95W11<br>5 Q9GZ28<br>5 Q9GZ28<br>5 Q8WT45<br>5 Q8T5F0<br>5 Q86LV7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 5 090676<br>5 081619<br>5 081519<br>5 081587<br>5 090685 |
| 223<br>2324<br>444<br>255<br>254 | 234<br>231<br>231<br>231              | 231<br>233<br>232<br>227<br>227                                                                                                 | 222<br>232<br>222<br>223<br>224<br>235<br>24<br>24                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 2229<br>2234<br>2234<br>2331<br>231                      |
| 50.9<br>50.8<br>49.1             | 966738                                | 4 4 4 4 4 4<br>0 7 4 4 4 4 6<br>0 0 0 0                                                                                         | 4 4 4 4 4 4 4 6 5 6 6 6 7 . L 4 4 4 7 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L 5 . L | 4807777                                                  |
| 654.5<br>654<br>653.5<br>631.5   |                                       | 579.5<br>578.5<br>574.5<br>569.5                                                                                                | 561.5<br>561.5<br>549.5<br>536.5<br>534                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 529.5<br>529.5<br>527.5<br>516.5<br>488.5                |
| 17<br>18<br>19                   | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | 3 3 5 5 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6 6                                                                                         | 332<br>332<br>342<br>344<br>347                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 0 6 4 4 4 4 4 4<br>0 0 0 1 4 6 4 6                       |

#### ALIGNMENTS

|                  |              |                 |                  |                    |                         |                     |                                               |                                |                   |     |                    |                                    |                                                                  |                                                                |                                 |              |                  |                             |                                   |                                |                            |                        |              |                         |                               | 0;                                                     | 09                                                             | 61                                                             | 120                                                          | 121             |
|------------------|--------------|-----------------|------------------|--------------------|-------------------------|---------------------|-----------------------------------------------|--------------------------------|-------------------|-----|--------------------|------------------------------------|------------------------------------------------------------------|----------------------------------------------------------------|---------------------------------|--------------|------------------|-----------------------------|-----------------------------------|--------------------------------|----------------------------|------------------------|--------------|-------------------------|-------------------------------|--------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------|--------------------------------------------------------------|-----------------|
|                  | '; 221 AA.   | ed)             | sequence update) | annotation update) |                         |                     | Cnidaria; Anthozoa; Zoantharia; Scleractinia; |                                |                   |     |                    |                                    | Gurskaya N.G., Fradkov A.F., Terskikh A., Matz M.V., Labas Y.A., | Martynov V.I., Yanushevich Y.G., Lukyanov K.A., Lukyanov S.A.; | a source of far-red fluorescent |              |                  |                             | ; IEA.                            |                                | tein.                      |                        |              | 93F9F4B5C2003CB4 CRC64; | Score 1156; DB 5; Length 221; | rred. NO. 2.18-100;<br>3; Mismatches 5; Indels 0; Gaps | SVIAKOMIYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 6 | SVIAKQMTYKVYMSGTVNGHYFEVQGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS 6 | QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS | —ფ              |
|                  | PRT;         | Created)        | Last             | Last               |                         |                     | a; Ant                                        | ora.                           |                   |     |                    | 682051                             | , Ters                                                           | Y.G.,                                                          | a sou                           |              |                  | ï                           | thways                            | ke.                            | fl_pro                     |                        | protei       |                         |                               | m                                                      | GHYFEV                                                         | GHYFEV                                                         | KOSFPG                                                       | KQSFPE          |
|                  | PRELIMINARY; | (TrEMBLrel, 19, |                  |                    | comoprotein.            | •                   |                                               | Fungiina; Poritidae; Goniopora | 75301;            |     | M N.A.             | MEDLINE=21538626; PubMed=11682051; | 3., Fradkov A.F.                                                 | , Yanushevich                                                  | "GFP-like chromoproteins as     | ' :`.        | 507:16-20(2001). | EMBL; AF383156; AAL27542.1; | <pre>91; P:energy pathways;</pre> | InterPro; IPR009017; GFP_like. | R000786; Green_fl_protein. | 33; GFP; 1.            | 됝            | 221 AA; 24918 MW;       |                               | .tarity 96.4%;<br>Conservative                         | AKOMTYKVYMSGTVN                                                | AKQMTYKVYMSGTVN                                                | SSIPETKYPEDIPDYV                                             | SIPFTKYPEDIPDYV |
| JLT 1            | 095204       | 01-DEC-2001     | 01-DEC-2001      | 01-OCT-2003        | GFP-like chromoprotein. | Goniopora tenuidens | Eukaryota; Metazoa;                           | Fungiina; Po                   | NCBI TaxID=75301; | [1] | SEQUENCE FROM N.A. | MEDLINE=2153                       | Gurskaya N.G                                                     | Martynov V.I                                                   | "GFP-like ch                    | proteins(1). | FEBS Lett. 5     | EMBL; AF3831                | GO; GO:0006091;                   | InterPro; IF                   | InterPro; IPR000786;       | Pfam; PF01353; GFP; 1. | ProDom; PD01 | SEQUENCE 2              | Query Match                   | best Local Similarity<br>Matches 212; Conserv          | 1 SVI                                                          | 2 SVI                                                          | 61 QYG                                                       | 62 Q¥G          |
| RESULT<br>095P04 | DI A         | H               | DT               | H                  | DE                      | SO                  | 8                                             | ပ္ပ                            | ŏ                 | RN  | RP                 | RX                                 | R.A                                                              | RA                                                             | RI                              | RT           | R.               | DR                          | DR                                | DR                             | DR                         | DR                     | DR           | SO                      | ō,                            | ĎΞ                                                     | à                                                              | QQ                                                             | Š                                                            | qq              |

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Red fluorescent protein.
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 Query Match
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 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 181
 1 SVIAKOMIYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 60
 65
 Eukaryota, Metazoa; Cnidaria, Anthozoa; Zoantharia; Corallimorpharia;
Discosomatidae; Discosoma.
NCBI_TaxID=86600;
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGGHYLCEFKSTYKAKK
 Gaps
 Maiz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G., Maizellov M.L., Lukyanov S.A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF168419; AAF03369.1; -.
EMBL; AF168419; AAF03369.1; -.
PDB; 1GTX; 07-NOV-01.
PDB; 1GTX; 06-DBC-00.
GO; GO:0006091; P:energy pathways; IEA.
InterPro; IPR000917; GFP like.
InterPro; IPR0009786; Green_fl_protein.
 Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G., Markelov M.L., Lukyanov S.A.; "Fluorescent proteins from nonbioluminescent Anthozoa species."; Nat. Biotechnol. 17:969-973 (1999).
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVACRFFRVKSRH 230
 ---RTEGRH 221
 14;
 Length 225;
 Query Match 60.8%; Score 783; DB 5; Length 22: Best Local Similarity 63.0%; Pred. No. 2.2e-65; Matches 145; Conservative 27; Mismatches 44; Indels
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ProDom; PD013756; Green_fl_protein; 1.
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 182 PVKMPGYHYVDRKLDVTNHNIDYTSVEQCEISIARKPVVA 221
 Last sequence update)
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 230 AA
 225 AA
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 PRT;
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 MEDLINE=99436614; PubMed=10504696;
 (TrEMBLrel. 16, TrEMBLrel. 16, (TrEMBLrel. 25,
 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
 01-MAY-2000 (TrEMBLrel. 13,
 Fluorescent protein FP583.
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 01-MAR-2001
01-MAR-2001
01-OCT-2003
 Discosoma sp
 181
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 8X9060
 O9GTJ7
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 RESULT 3
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 61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 66 QYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVSQDSSLKDGCFIYEVKFI 125
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 65
 1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 60
 6 NVIKEFMRFKVRMEGTVNGHEFEIKGEGEGRPYEGHCSVKLMVTKGGPLPFAFDILSPQF
 Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Corallimorpharia,
Discosomatidae, Discosoma.
NCBI_TaxID=105400;
Discosoma sp. SSAL-2000.
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;
Discosomatidae; Discosoma.
 Gaps
 MEDLINE-99436614; PubMed=10504696; Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G., Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G., "Fluorescent M.V., Lukyanov S.A.; "Fluorescent proteins from nonbioluminescent Anthozoa species."; Nat. Biotechnol. 17:969-973 (1999).

EMBL; AR168420; AAR03370.1.; -GO; GO:0006091; P:energy pathways; IEA.

InterPro; IPR009017; GFP like.

InterPro; IPR009017; GFP like.

PRO1353; GFP; 1.

PRO1353; GFP; 1.

PRO1355; Green_fl_protein.

PRODOM; PD013756; Green_fl_protein; 1.

SEQUENCE 232 AA; 26435 MW; AA8F18EEE283CE4D CRC64;
 .
9
 Length 230;
 186 PSVQLPGYYYVDSKLDMTSHNEDYTVVEQYEKTQGRHHPFIKPL 229
 P-VKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIAR----KPV 218
 MEDLINE-20434599; PubMed-10981720;
Fradkov A.F., Chen Y., Ding L., Barsova B.V., Matz M.V.,
Lukyanov S.A.;
 42; Indels
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Fluorescent protein FP483.
 58.3%; Score 750; DB 5; 62.5%; Pred. No. 2.8e-62; iive 36; Mismatches 42;
 PRT;
 Best Local Similarity 62.5%
Matches 140; Conservative
 PRELIMINARY;
 NCBI_TaxID=137428;
 SEQUENCE FROM N.A.
 Discosoma striata.
 SEQUENCE FROM N.A.
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62 OYGNRVFTKYPDDIPDYFKQTFPEGYSWERIMAYEDQSICTATSDIKMEGDCFIYEIQFH 121
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 2 SVIKPIMEIKLRMQGVVNGHKFVIKGEGEGKDFEGTQTINLTVKEGAPLPFAYDILTSAF
 61 QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 Kelmanson I.V., Matz M.V.;
"Molecular Basis and Evolutionary Origins of Color Diversity in Great
"Molecular Basis and Evolutionary Origins of Color Diversity in Great
Star Coral Montastraea cavernosa (Scleractinia: Faviida).";
Mol. Biol. Evol. 20:1125-1132-1132(2003).
EMBL; AY181557; AA061603.1;
SEQUENCE 225 AA; 25827 MW; A600ADD716C5921E CRC64;
 1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 Montastraea cavernosa (great star coral).
Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Scleractinia,
Faviina, Faviidae, Montastraea.
Q963F5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein.
Green fluorescent protein.
Bukaryota; Metazoa; (great star coral).
Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia; Paviina; Faviidae; Montastraea.
 "Green fluorescent proteins in Caribbean Scleractinian corals."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AF34683; AAK62982.5; ...
GOG GO:0006091; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
DEG: CO:0006091; GFP_like.
DEG: CO:0006091; GFP_like.
 SEQUENCE FROM N.A.
Lesser M.P., Barry T.M., Mazel C., Matz M.V., Lukyanov S.A.
Falkowski P., Gorbunov M., Kolber Z.,
 Length 225;
 Length 225;
 52; Indels
 48; Indels
 PERM; PF01353; GFP; 1.
PRINTS; PR01229; GFLUORESCENT.
ProDom; PD013756; Green fl protein; 1.
SEQUENCE 225 AA; 25847 MW; 77DE7D7C616929AF CRC64;
 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein.
 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIAR 215
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MEDLINE=22689801; PubMed=12777529;
 PRT;
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 Query Match
Best Local Similarity 56.7%
Matches 122; Conservative
 Matches 121; Conservative
 PRELIMINARY;
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 NCBI_TaxID=63558;
 Q7Z0W4
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 QYGNXAFVHHPDNIHDYLKLSFPEGYTWERSMHFEDGGLCCITNDISLTGNCFYYDIKFT 125
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 GLNFPPNGFVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGGHYLCEFKSTYKAKK 180
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 61
 SVIKEEMLIDLHLEGTFNGHYFEIKGKGKGOPUEGTNTVTLEVTKGGPLPFGWHILCPQF 65
 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 60
 2 NLIKEDMRVKVHMEGNVNGHAFVIEGEGKGRPYEGTQTLNLTVKEGAPLPFSYDILTTAL
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK
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 0; Gaps
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 MEDLINE=21927629; PubMed=11929996;
Labas Y.A., Gurskaya N.G., Yanushevich Y.G., Fradkov A.F.,
Lukyanov K.A., Lukyanov S.A., Matz N.V.;
"Diversity and evolution of the green fluorescent protein family.";
Proc. Natl. Acad. Sci. U.S.A. 99:4256-4261(2002).
 Green fluorescent protein.
Dendronephthya sp. SSAL-2002.
Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Alcyonacea;
Nephtheidae; Dendronephthya.
 1;
 57.3%; Score 737.5; DB 5; Length 232; 60.2%; Pred. No. 4.2e-61; ive 38; Mismatches 47; Indels 1
 Length 236;
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55.8%; Pred. No. 3.1e-58;
ive 45; Mismatches 50; Indels
 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 181 -PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIAR 215
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIAR 215
 225 AA
 236 AA
 "Diverary Natl. Acad. Sci.
EMBL; AF420591; AAM10625.1; -...
GO; GO:006691; P:energy pathways; IEA.
InterPro; IPR009017; GFP_like.
InterPro; IPR000786; Green_fl_protein.
 PRT;
 PRT;
 120; Conservative
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 PRELIMINARY;
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 Similarity
 Query Match
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 NCBI_TaxID=191210;
 SEQUENCE FROM N.A.
 01-JUN-2002
01-JUN-2002
 181
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Best Local
 Q8T6U0;
 Q963F5
 QSTGUO
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YGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFSG 121
 105 YGNRALTKYPDDIADYFKQSFPEGYSWERTMTFEDKGIVKVKSDISMEEDSFIYEIRFDG 164
 61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQ---GNCFIYHV 117
 Kelmanson I.V., Matz M.V.;
"Molecular Basis and Evolutionary Origins of Color Diversity in Great
Molecular Basis and Evolutionary Origins of Color Diversity in Great
Star Coral Montastraea cavernosa (Scleractinia: Faviida).";
Star Coral Bvol. 20:1125-1133 (2003).
EMBL; AX181555; AA061661.1; .
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 2 VIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQCQ
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 MEDLINE=99436614; PubMed=10504696;
Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G.,
Markelov M.L., Lukyanov S.A.;
 Montastraea cavernosa (great star coral).
Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Scleractinia,
Faviina, Faviidae, Montastraea.
 "Fluorescent proteins from nonbioluminescent Anthozoa species.";
 Nat. Biotechnol. 17:969-973(1999).

EMBL; AF16844; AAF03374.1; -
GO: GO:0006091; P:energy pathways; IEA.

InterPro; IPR009017; GFP like.

InterPro; IPR009017; GFP like.

InterPro; IPR00186; Green fl protein.

Pram; PP01353; GFP; 1.

PRINTS; PR01229; GFP; 1.

PRODOM; PD013766; Green fl protein; 1.

SEQUENCE 266 AA; 30450 MW; B4E97406E2708854 CRC64;
 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein.
 Score 671; DB 5;
Pred. No. 8.6e-55;
7; Mismatches 58
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225 VKL.PDYHFVDHRIEILNHDKDYNKVTLYENAVAR 258
 182 VKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIAR 215
 52.0%; Score 669.5; DB 5 54.9%; Pred. No. 9.8e-55; ive 41; Mismatches 52
 227 AA
 PRT;
 STRAIN=mc4;
MEDLINE=22689801; Pubmed=12777529;
 52.1%; Sco
55.6%; Pre-
tive 37;]
 Best_Local Similarity 54.9%
Matches 117; Conservative
 Conservative
 PRELIMINARY;
 Sest Local Similarity
Matches 119; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=63558;
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 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
 181
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCBFKSTYKAKK 180
 61
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2 SVIKSVMKIKLHMDGIVNGHKFMITGEGEGRPFEGTHTIILKVKEGGPLPFAYDILTTAP
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 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 MEDILIND-LACULOS...
Kelmanson I.V., Matz M.V.;
"Molecular Basis and Evolutionary Origins of Color Diversity in Great
"Notecular Montastraea cavernosa (Scleractinia: Faviida).";
 Gaps
 Cyan fluorescent protein.

Cyan fluorescent protein.

Cyan fluorescent protein.

Bundrastraca cavernosa (great star coral).

Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia; Faviina; Faviina; Faviina; Montastraca.
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 Bukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Alcyonacea;
Clavulariidae; Clavularia.
NCBI_TaxID=86521;
 Length 225;
 52.4%; Score 674; DB 5; Length 22 54.9%; Pred. No. 3.7e-55; Indels ive 42; Mismatches 55; Indels
 .556; AAU616U2.1; -.
225 AA; 25843 MW; 13708587B7D93E35 CRC64;
 (Tremblrel. 25, Created)
(Tremblrel. 25, Last sequence update)
(Tremblrel. 25, Last annotation update)
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Fluorescent protein FP484.
Clavularia sp.
 |::| ||:|| :::::|:|| :|: || SVQLPDYHFVDHRIEILSHDNDYNTVKLSENAEAR 216
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIAR 215
 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIAR 215
 | : | | | : | | : : : : | : | | : | | GVVLPEYHEVDHRIEILSHDKDYNTVEVYENAVAR
 Ā
 266 AA
 Star Coral Montastraea cavernosa (Sc)
Mol. Biol. Evol. 20:1125-1133(2003).
EMBL; AX181556; AAO61602.1; -.
 PRT;
 MEDLINE=22689801; PubMed=12777529;
 Best Local Similarity 54.9
Matches 118; Conservative
 PRELIMINARY;
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 [1]
SEQUENCE FROM N.A.
 01-OCT-2003
 01-OCT-2003
 01-OCT-2003
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 121
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 Q9U6Y3;
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61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQ---GNCFIYHV 117
 62 DYGNRVFAKYPQDIPDYFKQTFPEGYSWERSMTYEDQGICVATNDITLMKGVDDCFVYKI 121
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 2 SVIXPDMKIKLRMEGAVNGHKFVIEGDGKGKPFEGTQSMDLTVKEGAPLPFAXDILTTVF
 Kelmanson I.V., Matz M.V.;
"Molecular Basis and Evolutionary Origins of Color Diversity in Great Star Coral Montestraea cavernosa (Scleractinia: Favilda).";
Mol. Biol. Evol. 20:1125-1133(2003).
EMBL; AY81553; AAO61599.1; -
SEQUENCE 227 AA; 26017 MW; 5E312C54EA47FS89 CRC64;
 2 SVIKPDMKIKLRMEGAVNGHKFVIEGDGKGKPFEGTQSMDLTVKEGAPLPFAYDILTTVF
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 Montastraea cavernosa (great star coral).
Sukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Scleractinia,
Faviina, Faviidae, Montastraea.
NCBI_TaxID=63558;
 DB 5; Length 227;
Pfam; PF01353; GFP; 1.
ProDom; PD013756; Green fl protein; 1.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Green fluorescent protein.
 51.9%; Score 667.5; DB 5; 54.9%; Pred. No. 1.5e-54; ative 40; Mismatches 53;
 53;
 51.9%; Score 667.5; DB 5 54.9%; Pred. No. 1.5e-54;
 178 AKKPVKMPGYHYVDRKLDVTNHNKDYTSVEQCE 210
 178 AKKPVKMPGYHYVDRKLDVTNHNKDYTSVEQCE 210
 ||| |::| ||:|| |::| AKKFVQLPDYHFVDHRIEILSHDKDYNKVKLYE 214
 Z
 40; Mismatches
 PRT;
 PRT;
 MEDLINE=22689801; PubMed=12777529;
 Best Local Similarity 54.9%
Matches 117; Conservative
 Conservative
 PRELIMINARY;
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 Query Match
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Matches 117; Conserv
 SEQUENCE FROM N.A. STRAIN=mc2;
 Q7Z0W8;
01-OCT-2003
01-OCT-2003
 182
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 61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180
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Kelmanson I.V., Matz M.V.;
"Molecular Basis and Evolutionary Origins of Color Diversity in Great
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 Red fluorescent protein.
Montastraea cavernosa (great star coral).
Bukaryota; Metazoa; Gnidaria; Anthozoa; Zoantharia; Scleractinia;
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 Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
Faviina; Paviidae; Montastraea.
 SEQUENCE FROM N.A.
Lesser M.P., Barry T.M., Mazel C., Matz M.V., Lukyanov S.A.,
Lesser M.P., Borry T.M., Kolber Z.;
Eaklowski P., Gorbunov M., Kolber Z.;
Streen Fluorescent Proteins in Caribbean Scleractinian Corals.";
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF401282; AAK83923.1;
 51.9%; Score 667.5; DB 5; Length 225; 55.5%; Pred. No. 1.5e-54; Live 40; Mismatches 53; Indels 1;
 225 AA; 25822 MW; 830871F6936953E2 CRC64;
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Green fluorescent protein.
 01-OCT-2003 (TrEMBLrel. 25, Created)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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 Star Coral Montastraea cavernosa (Sc)
Mol. Biol. Evol. 20:1125-1133(2003).
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MEDLINE=22689801; PubMed=12777529;
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 NCBI_TaxID=48498;
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Montastraea everenosa (great star coral).
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EMBL; AYO65460; AALJ7905.1;
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 820C89437F8BDB32 CRC64;
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ProDom; PD013756; Green_fl_protein; 1.
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ProDom; PD013756; Green fl protein; 1.
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 Gaps
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Pred. No. 1.6e-53;
 181 P-VKMPGYHYVDRKLDVTNHNKDYTSVEQCE 210
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Copyright (c) 1993 - 2004 Compugen Ltd.
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| Title:              | US-09-890-463-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                          |
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Sequence: 1 SVIAKQMTYKVYMSGTVNGH.....SIARKPLVACCFFRVKSRHK 231

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 1586107

1586107 segs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*
1: geneseqp1980s:\*
2: geneseqp2090s:\*
3: geneseqp2000s:\*
5: geneseqp2001s:\*
6: geneseqp2002s:\*
7: geneseqp2003as:\*
7: geneseqp2003bs:\*
8: geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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#### ALIGNMENTS

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Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 N-terminal; pigment protein from coral tissue; PPCT; fluorescence; tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet; UV filter; POC3.
 /note= "critical residue in the vicinity of the fluorophore"
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 'note= "critical residue in the vicinity of
 61. .63
/label= Chromophore_motif
 Pigment protein from coral tissue POC3.
 Location/Qualifiers
 AAY97149 standard; protein; 231 AA
 02-FEB-2000; 2000WO-AU000056.
 99AU-00008463.
 fluorophore"
 fluorophore' Misc-difference 210
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 (UNSY) UNIV SYDNEY.
 WPI; 2000-532892/48.
N-PSDB; AAA52082.
 Misc-difference 158
 Misc-difference 192
 Hoegh-Guldberg O,
 Misc-difference 61
 Acropora aspera.
 WO200046233-A1.
 02-FEB-1999;
 04-DEC-2000
 10-AUG-2000.
 AAY97149;
RESULT 1
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Query Match
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 181
 AAY97150;
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 QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 GLNFPPNGPVMQKKTQGWEDNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 cDNA libraries were constructed from a blue pigmented coral, Acropora sequences encoding polypeptides with N-terminal sequences as shown in AAV97147-48. Pigment protein from coral tissue (PPCT) is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dysetuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters (both
 9
 1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
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 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRHK 231
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 201.
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 Mismatches
Claim 13; Page 42-43; 49pp; English.
 ABP70025 standard; protein; 231 AA
 Brugliera F,
Prescott M;
 0;
 100.0%;
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 02-MAR-2001; 2001US-0273227P
 (first entry)
 Query Match 100.
Best Local Similarity 100.
Matches 231; Conservative
 QUEENSLAND.
 (revised)
 Karan M,
 WPI; 2002-740765/80
 sink; sunscreen.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 (NUFA-) NUFARM LID.
 JONES E L.
 Sequence 231 AA;
 WO200270703-A2
 VIND
 Unidentified
 06-AUG-2003
 22-JAN-2003
 12-SEP-2002.
 181
 ABP70025;
 61
 121
 121
 181
 (UYQU)
 claimed
 ABP70025
XX
AC ABP7
XX
AC ABP7
XX
DT 22-5
DT 22-5
DT 22-5
XX
COL(
XW
C
 RESULT
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The invention relates to an isolated colour-facilitating molecule (CFW)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

cransgenic animal which exhibits a novel colour e.g. sheep with blue or

cransgenic animal which exhibits a novel colour e.g. sheep with blue or

cransgenic animal which exhibits a novel colour e.g. sheep with blue or

cractions and coloured fleece. They are useful for producing agent. Other

costing materials that experience UV damage e.g. plastics and car

clight for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

clight for growing phototropic organisms e.g. algae and/or crals, for

coating materials that experience UV damage e.g. plastics and car

coating markers, general reporter molecules, photon traps, UV sinks

coating markers, general reporter molecules, photon traps, UV sinks

coating markers, and in fruits and vegetables to enhance their

chungal species, and in fruits and vegetables to enhance their

characteris of distorted light spectra (Diomatrix). The first all-protein

chromophore to be isolated was Green Fluorescent protein (GFP). The

sequences given in records ABB69924-ABP7048 represent CFM related amino

coating acquences given in records ABG9024-ABP7048 represent CFM related amino
 120
 61 QYGSIPFTKYPEDIPDYVKQSFFGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 GLNFPPNGPVMOKKTOGWEPNTERLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKARK 180
 121 GLNFPPNGFVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 9
 09
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 Gaps
 fluorescent marker; dyestuff; sunscreen; ultra violet;
 N-terminal; pigment protein from coral tissue; PPCT; fluorescence;
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRHK 231
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRHK 231
 .
 /note= "critical residue in the vicinity of the
 Length 231;
 Indels
 100.0%; Score 1268; DB 5; 100.0%; Pred. No. 1.3e-128;
 .
0
 0; Mismatches
 Misc-difference 61. .63
/label= Chromophore_motif
 Pigment protein from coral tissue POC4.
 Location/Qualifiers
 Ą.
 6; Page 478; 510pp; English
 AAY97150 standard; protein; 235
 (first entry)
 Best_Local Similarity 100.
Matches 231; Conservative
 Misc-difference 158
 Sequence 231 AA;
 Acropora aspera.
 marker;
 04-DEC-2000
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o:
 120
 120
 180
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 aspera to isolate sequences encoding polypeptides with N-terminal aspera to isolate sequences encoding polypeptides with N-terminal sequences as shown in AAV97147-48. Pigment protein from coral tissue (PPCT) is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 100-700 nm. PPCT may be expression in transformed tissues) or general dysetuff (all claimed).
 9
 9
 Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKAKK
 1 SVIAKOMIYKVYMSGIVNGHYFEVEGDGKGKPYEGEQIVRLAVIKGGPLPFAWDILSPQC
 QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 0; Gaps
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRHK 231
 'note= "critical residue in the vicinity of the
 Score 1242; DB 3; Length 235;
Pred. No. 8.9e-126;
2; Mismatches 2; Indels
 /note= "critical residue in the vicinity of fluorophore"
 Claim 13; Page 43-44; 49pp; English.
 97.9%;
 02-FEB-2000; 2000WO-AU000056
 99AU-00008463
 fluorophore"
fluorophore"
 Dove S;
 227; Conservative
 WPI; 2000-532892/48.
 (UNSY) UNIV SYDNEY
 Similarity
 Hoegh-Guldberg O,
 N-PSDB; AAA52083.
 Sequence 235 AA;
 Misc-difference
 Misc-difference
 WO200046233-A1
)2-FEB-1999;
 181
 61
 121
 181
 61
 Query Match
Best Local
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the ocell when visualised by a human ew in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel coloure e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs embedded in a gel matrix improve image quality in marketability. CFMs embedded in a gel matrix improve image quality in the sequences given in records ABB69924-ABP70048 represent CFM related amino
 120
 120
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 9
 9
 characteristics to cells in the absence of excitation by extraneous non-white light.
 1 SVIAKQMIYKVIMSGIVINGHYFEVBGDGKGKPYBGBQIVRLAVIKGGPLPFAWDILSPQC
 61 QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 Gaps
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual
Colour facilitating molecule; CFM; green fluorescent protein; GFP; detromophore; blomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen.
 ·.
 Length 235;
 Indels
 Dove SG;
 97.9%; Score 1242; DB 5; 98.3%; Pred. No. 8.9e-126; ive 2; Mismatches 2;
 Brugliera F, Mason J,
Prescott M;
 Example 20; Page 502-503; 510pp; English.
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 Matches 227; Conservative
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80
 Local Similarity
 (UYQU) UNIV QUEEN (JONE/) JONES E L.
 Sequence 235 AA;
 WO200270703-A2
 12-SEP-2002
 Н
 Query Match
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Colour Facilitating molecule (CFM) related sequence #SEQ ID 245.

(first entry)

22-JAN-2003

ABP70042;

ABP70042 standard; protein; 235 AA

us-09-890-463-3.rag

0

Gaps

0;

9

Mismatches

2,

Matches 223; Conservative

Similarity

Query Match Best Local &

Length 235 Indels

Score 1212; DB 5; Pred. No. 1.6e-122;

95.6%;

9 09 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120

QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKRS

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61 61

1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC

GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180 121 GLNFPPNGPVMQKKTQGWEPNTBRLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKAKK 180

121

PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRVKSRHK 231

181 181

ABP70037 standard; protein; 220 AA

RESULT 6 ABP70037

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Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 PUKWPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVACRFFRVKSRHK 231
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 202
PVKMPGYHYVDRKLDVTNHNKDYTSVEOREISIARKPLVACCFFRVKSRHK
 Dove SG;
 Mason J,
 Brugliera F,
Prescott M;
 ABP70026 standard; protein; 235 AA
 Claim 5; Page 479; 510pp; English.
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 (first entry)
 (NUFA-) NUFARM LID.
(UYQU) UNIV QUEENSLAND.
(JONE/) JONES E L.
 (revised)
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80.
 UV sink; sunscreen
 WO200270703-A2
 Unidentified
 06-AUG-2003
 12-SEP-2002.
 22-JAN-2003
 white light
 ABP70026;
 181
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Colour facilitating molecule, CFM; green fluorescent protein, GFP, chromophore, biomatrix; transgenic animal, colouring agent, flower industry, expression marker, reporter molecule, photon trap;

UV sink; sunscreen

WO200270703-A2

12-SEP-2002

Unidentified

02-MAR-2001; 2001US-0273227P. 21-MAR-2001; 2001AU-00003874. 15-OCT-2001; 2001US-0329816P.

(NUFA-) NUFARM LTD. (UYQU ) UNIV QUEENSLAND.

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(UYQU ) UNIV Q (JONE/) JONES

01-MAR-2002; 2002WO-GB000928

Colour Facilitating molecule (CFM) related sequence #SEQ ID 239.

(revised)
(first entry)

06-AUG-2003 22-JAN-2003

ABP70037;

The invention relates to an isolated colour-facilitating molecule (CFM)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

ransgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing coloured plant

red coloured fleece. They are useful for producing agent. Other

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

cating materials that experience UV damage e.g. plastics and car

light for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

coating materials that experience of the contemplated uses include,

coating materials reporter molecules, photon traps, UV sinks or

new varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

fungal species, and in fruits and vegetables to enhance their

marketability. CFMs embedded in a gel matrix improve image quality in

situations of distorted light spectra (blomatrix). The first all-protein

chromophore to be isolated was Green Flores ent protein (GFP). The

chromophore to be isolated was Green Flores ent groen in GFP). The

sequences given in records ABB66924-ABP71048 represent CFM related amino

Sequence 235 AA;

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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured called they are useful for producing settracts, e.g. flavouring, beverage or juice or colouring agent. Other
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Dove SG;
 Mason J,
 Example 19; Page 497-498; 510pp; English.
 Brugliera F,
 Prescott M;
Karan M,
 WPI; 2002-740765/80
 Hoegh-Guldberg IO,
 white light.
 EL.
 Jones
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ö uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CEMS are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CEMS modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CEMS embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP6924-ABP70048 represent CEM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.) 120 180 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180 9 09 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYBGEQTVRLAVTKGGPLPFAMDILSPQC 61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS GLNF PPNGPVMQKKTQGWEPNTERLFARDGML1GNNFMALKLEGGGHYLCEFKSTYKARK 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC Gaps Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; Colour Facilitating molecule (CFM) related sequence #SEQ ID 238. . 0 94.8%; Score 1202; DB 5; Length 220; llarity 100.0%; Pred. No. 1.7e-121; Conservative 0; Mismatches 0; Indels 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVA 220 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVA 220 Dove SG; Mason J, ABP70036 standard; protein; 226 AA Brugliera F, Prescott M; 21-MAR-2001; 2001AU-00003874. 15-OCT-2001; 2001US-0329816P. 01-MAR-2002; 2002WO-GB000928. 02-MAR-2001; 2001US-0273227P. (revised)
(first entry) UNIV QUEENSLAND Karan M, WPI; 2002-740765/80 flower industry; ex UV sink; sunscreen. Hoegh-Guldberg IO, (UYQU ) UNIV QUEEN! (JONE/) JONES E L. Similarity (NUFA-) NUFARM LTD Sequence 220 AA; 40200270703-A2 Unidentified 06-AUG-2003 22-JAN-2003 220; 12-SEP-2002 ABP70036; Jones EL, Query Match Local Best Loca Matches RESULT 7 ABP70036 g ð g à g ∂

The invention relates to an isolated colour-facilitating molecule (CFM)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

non-white light or particle emission. CFMs are useful for producing a

cransgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing coloured plant

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

cuses include transducing or intensifying an image, providing additional

light for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

upholstery. CFMs are useful in the flower indusery, in the development of

new varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs embedded in a gel matrix improve image quality in

customers. CFMs embedded in a gel matrix improve image quality in

situations of distorted light specira (biomatrix). The first all-protein

chromophore to be isolated was Green Fluorescent protein (GFP). The

sequences given in records ABP69924-ABP0048 represent 120 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 180 9 9 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS 61 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 61 QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS Gaps Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; ·; Colour Facilitating molecule (CFM) related sequence #SEQ ID 54 acid sequences. (Updated on 06-AUG-2003 to correct OS field.) Length 226; Indels PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVACCFFRV 9 Score 1184; DB 5; Pred. No. 1.6e-119; 3; Mismatches Example 19; Page 496-497; 510pp; English. ABP69941 standard; protein; 220 AA 93.4%; 96.0%; (first entry) Matches 217; Conservative Local Similarity UV sink; sunscreen. Sequence 226 AA; WO200270703-A2 22-JAN-2003 white light 181 ABP69941; 181 Query Match RESULT 8 ABP69941 à g à g ð d ð 셤 

12-SEP-2002

0

Facilitating molecule (CFM) related sequence #SEQ ID

22-JAN-2003 (first entry)

Colour

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0
 The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle ewission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensitying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of marging materials plantes. Other contemplated uses include,
 expression markers, general reporter molecules, photon traps, UV sinks or in unscreens. CPMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of disported light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABF69924-ABP70048 represent CFM related amino
 120
 120
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKARK 180
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 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 SVIAKOMIYKVYMSGIVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 Gaps
 .;
0
 Length 220;
 4; Indels
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVA 220
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA 220
 Dove SG;
 Score 1170; DB 5;
Pred. No. 5.1e-118;
1; Mismatches 4;
 Mason J,
 Claim 5; Page 330-331; 510pp; English.
 Brugliera F,
 Prescott M;
 01-MAR-2002; 2002WO-GB000928.
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 2001US-0273227P
 92.3%;
 Matches 215; Conservative
 QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 Hoegh-Guldberg 10,
 (NUFA-) NUFARM LTD
 JONE/) JONES E L.
 Best Local Similarity
 Sequence 220 AA;
 acid sequences
 02-MAR-2001;
 21-MAR-2001;
 white light,
 Jones EL,
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 61
 181
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 121
 181
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The invention relates to an isolated colour-facilitating molecule (CFM)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

non-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing coloured plant

est include transducing or intensifying an image, providing additional

light for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

upholstery. CFMs are useful in the flower industry, in the development of

new varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs embedded in a gel matrix improve image quality in

situations of distorted light spectra (biomatrix). The first all-protein

chromophore to be isolated was Green Fluorescent protein (GFP). The

sequences given in records ABBP69924-ABP70048 represent CFM related amino
 QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIXHVKFS 120
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 09
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 SVIAKOMIYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPQS
 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 flower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen.
Colour facilitating molecule, CFM, green fluorescent protein, GFP, chromophore, biomatrix, transgenic animal, colouring agent,
 ·,
 Length 220;
 Indels
 Dove SG;
 Score 1170; DB 5;
Pred. No. 5.1e-118;
 Mason J,
 Pred. No. 5.1e
1; Mismatches
 Claim 5; Page 327-328; 510pp; English.
 Brugliera F,
Prescott M;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928.
 92.3%;
 Sest Local Similarity 97.7
Matches 215; Conservative
 (NUFA-) NUFARM LTD.
 Karan M,
 WPI; 2002-740765/80
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 Sequence 220 AA;
 (UYQU) UNIV QUE
(JONE/) JONES E
 WO200270703-A2
 acid sequences
 Millepora sp.
 12-SEP-2002
 white light
 61
 61
 Query Match
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ABP69940 standard; protein; 220 AA.

ABP69940;

ABP69940 ID ABP6 XX AC ABP6 RESULT 9

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acid sequences
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 The invention relates to an isolated colour-facilitating molecule (CFM)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

non-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing coloured plant

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

uses include transducing or intensifying an image, providing additional

city for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

cupholstery. CFMs are useful in the flower industry, in the development of

new varieties of flowering plants. Other contemplated uses include,

captression markers, general reporter molecules, photon traps, UV sinks or

conting markers, general reporter molecules, photon traps, UV sinks or

conting species, and in fruits and vegetables to enhance their

cundal species, and in fruits and vegetables to enhance their

chromophore to be isolated was Green Fluorescent procein (GFP). The

chromophore to be isolated was Green Fluorescent procein (GFP). The

sequences given in records ABP69924-ABP70048 represent CFM related amino
 121 GLNFPPNGPVMQKKTQGWEDNTERLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKARK 180
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID
 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPVVA 220
 Dove SG;
 Mason J,
 Claim 5; Page 325-326; 510pp; English
 ABP69939 standard; protein; 220 AA
 Brugliera F,
 Prescott M;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928.
 (first entry)
 OUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 Hoegh-Guldberg IO,
 UV sink; sunscreen
 NUFA-) NUFARM LTD
 (UYQU) UNIV QUEEN
(JONE/) JONES E L.
 WO200270703-A2
 Millepora sp.
 22-JAN-2003
 white light.
 12-SEP-2002.
 Jones EL,
 ABP69939;
 181
 RESULT 10
 ABP69939
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 The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a
 120
 120
 121 GINFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 09
 09
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 61 QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 61 QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 1 SVIAKOMIYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPQS
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 0;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 22
 Length 220;
 4; Indels
 PVKMPGYHYVDRKLDVTMHNKDYTSVEQREISIARKPVVA 220
 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVA 220
 Dove SG;
 Score 1167; DB 5;
Pred. No. 1.1e-117;
2; Mismatches 4;
 Mason J,
 Claim 5; Page 286-287; 510pp; English.
 AA.
 Brugliera F,
Prescott M;
 ABP69925 standard; protein; 220
 01-MAR-2002; 2002WO-GB000928.
 02-MAR-2001; 2001US-0273227P.
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 92.0%;
 (first entry)
 Conservative
 (NUFA-) NUFARM LTD. (UYQU) UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 flower industry; ex
UV sink; sunscreen.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 Similarity
 (UYQU) UNIV QUE
(JONE/) JONES E
Sequence 220 AA;
 WO200270703-A2.
 22-JAN-2003
 12-SEP-2002
 white light
 Local Simi
tes 214;
 ABP69925;
 Query Match
 Matches
 RESULT 11
ABP69925
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transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental tungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light species (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 ·,
 120
 120
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 GLNFPFNGPVMQKKTQGWEPNTERLLARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 9
 9
 1 SVIAKOMIYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 SVIAKOMIYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLTVTKGGPLPFAWDILSPOS
 QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; blomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen.
 ;
0
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 32.
 Length 220;
 Indels
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVA 220
 PVKMPGYHYVDRKLDVINHNKDYTSVEQREISIARKFVVA 220
 5.
 Score 1164; DB 5;
Pred. No. 2.3e-117;
1; Mismatches 5;
 ABP69930 standard; protein; 220 AA
 91.8%;
97.3%;
 2001US-0273227P.
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 (first entry)
 Matches 214; Conservative
 QUEENSLAND.
 (revised)
 Karan M,
 Query Match
Best Local Similarity
 (NUFA-) NUFARM LTD
 JONES E L.
 Sequence 220 AA;
 acid sequences
 WO200270703-A2
 Caulastrea sp
 UNIV
 02-MAR-2001;
 06-AUG-2003
22-JAN-2003
 12-SEP-2002
 ABP69930;
 Н
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 121
 181
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(JONE/)
 RESULT 12
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Dove SG;

Mason J,

Brugliera F,

Jones EL,

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The invention relates to an isolated colour-facilitating molecule (CFW)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

cransgenic animal which exhibits a novel colour e.g. sheep with blue or

cransgenic animal which exhibits a novel colour e.g. sheep which blue or

cractions and the ransducing or intensifying an image, providing agent. Other

cases include transducing or intensifying an image, providing additional

clight for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics and car

coating markers, general reporter molecules, photon traps, UV sinks or

coating markers, general reporter molecules, photon traps, UV sinks or

coating markers, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in

chromophore to be isolated was Green Fluorescent protein

chromophore to be isolated was Green Fluorescent protein

chromophore to be isolated was Green Fluorescent germences given in records ABB69924-ABP70048 represent CFM related amino
 ö
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 120
 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 121 GLNFPPNGPVMQKKTQGWEPNTERLSARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 09
 9
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 61 QYGSIPFIKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 1 SVIAKOMTYKVYMSGTVNGHYPEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 SVIAKQMIYKVYMSGIVNGHYFEVEGDGKGKPYEGEQTVRLIVTKGGPLPFAMDILSPQS
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; blomatrix; transgenic animal; colouring agent; lower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen.
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 220.
 ..
 Length 220;
 Indels
 PUKMPGYHYVDRKLDVTNHNKDYTSVEOREISIARKPVVA 220
 PVKMPGYHYVDRKLDVINHNKDYTSVEQREISIARKPLVA 220
 91.6%; Score 1162; DB 5;
97.3%; Pred. No. 3.8e-117;
iive 1; Mismatches 5;
 Claim 5; Page 298-299; 510pp; English.
 ABP70032 standard; protein; 223 AA
 1,
 (first entry)
 Matches 214; Conservative
 WPI; 2002-740765/80
Hoegh-Guldberg IO,
 Local Similarity
 Sequence 220 AA;
 22-JAN-2003
 Sinularia sp.
 white light
 61
 121
 ABP70032;
 181
 Query Match
 181
 RESULT 13
 ABP70032
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WO200270703-A2

ABP69926 standard; protein; 220 AA.

ABP69926,

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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the ore when visualised by a human ey in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant or arrangement of the extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules photon traps, UV sinks or in sunscreens. CFMs embedded in a gel matrix improve image quality in the flowering or situations of distorted light spectra (bomatrix). The first all-procein chromophore to be isolated was Green Fluorescent procein (GFP). The sequences given in records ABB69924-ABP70048 represent CFM related amino
 121 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 GLNFPPNGPVMQKKTQGWEDNTERLFARDGMLIGNNFWALKLEGGGHYLCEFKSTYKAKK 181
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-white light.
 SVIAKOMTYKVYMSGTVNGHYPEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 61 QYGSIPFIKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 QYGSIPFTKYLEDIPDYVKQSFPEGFTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 1 SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 91.6%; Score 1162; DB 5; Length 223; 97.3%; Pred. No. 3.8e-117; ive 2; Mismatches 4; Indels
 181 PVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKPLVA 220
 182 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPLVA 221
 Dove SG;
 Mason J,
 Disclosure; Page 489; 510pp; English.
 Brugliera F,
Prescott M;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 97.3%;
 Matches 214; Conservative
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80
 Local Similarity
 (JONE/) JONES E L.
 Sequence 223 AA;
 12-SEP-2002
 62
 Query Match
 (UYQU
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 à
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The invention relates to an isolated colour-facilitating molecule (CFM)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

coloured fleece. They are useful for producing coloured plant

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

cextracts, e.g. flavouring, beverage or juice or colouring agent. Other

uses include transducing or intensifying an image, providing additional

light for growing phototropic organisms e.g. algae and/or corals, for

coating meterials that experience UV damage, providing additional

coating materials that experience UV damage e.g. plastics and car

coating markers, general in the flower industry, in the development of

men varieties of flowering plants. Other contemplated uses include,

corression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs modify visible colour in edible and/or conamental

constitutions of distorted light speciex (biomatrix). The first all-protein

chromophore to be isolated was Green Fluorescent protein (GFP). The
 chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVRLAVTKGGPLPFAWDILSPQC
 1 SVIAKOMIYKVYMSGIVNGHYFEVEGDGKGKPYEGEQTVRLIVIKGGPLPFAMDILSPQS
 Gaps
 Colour facilitating molecule, CFM; green fluorescent protein; GFP; chromophore, biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 ·;
 91.2%; Score 1156; DB 5; Length 220; 96.4%; Pred. No. 1.7e-116; ive 3; Mismatches 5; Indels
 Colour Facilitating molecule (CFM) related sequence #SEQ ID
 Dove SG
 Mason J,
 Brugliera F,
 Claim 5; Page 289; 510pp; English.
 Prescott M;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 (first entry)
 Matches 212; Conservative
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 WPI; 2002-740765/80
 Karan M,
 UV sink; sunscreen.
 Hoegh-Guldberg IO,
 Query Match
Best Local Similarity
 JONE/) JONES E L.
 Sequence 220 AA;
 Acropora aspera.
 WO200270703-A2.
 12-SEP-2002
 22-JAN-2003
 white light
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Gaps

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9 61 120 121

> RESULT 14 ABP69926

ö 9 09 chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino

Sequence 223 AA; acid sequences

88888

situations of distorted light spectra (biomatrix). The first all-protein

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GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFWALKLEGGGGHYLCEFKSTYKARK 180
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS
 industry; expression marker; reporter molecule; photon trap;
 Colour facilitating molecule, CFM, green fluorescent protein, GFP, chromophore, biomatrix, transgenic animal, colouring agent,
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 216.
 PVKMPGYHYVDRKLDVTNHNKDYTSVEOREISIARKPLVA 220
 Dove SG;
 Mason J,
 Jones EL, Karan M, Brugliera F,
Hoegh-Guldberg IO, Prescott M;
 ABP70030 standard; protein; 223 AA
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928.
 (first entry)
 QUEENSLAND.
 WPI; 2002-740765/80.
 flower industry; e
UV sink; sunscreen
 (NUFA-) NUFARM LTD
 (UYQU) UNIV QUEEN
(JONE/) JONES E L.
 WO200270703-A2
 Tubastrea sp.
 22-JAN-2003
 12-SEP-2002.
 ABP70030;
61
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The invention relates to an isolated colour-facilitating molecule (CFW) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous con-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or ced coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower indusery, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in

Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-

Example 18; Page 486; 510pp; English

white light.

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GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKARK 180
 QYGSIPFTKYPEDIPDYVKQSFPGRYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 120
 QYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYHVKFS 121
 122 GLNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGHYLCEFKSTYKAKK 181
 09
 61
 1 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYBGEQTVRLAVTKGGPLPFAWDILSPQC
 SVIAKOMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPOS
 Gaps
 0;
 Length 223;
 Indels
 181 PVKMPGYHYVDRKLDVINHNKDYTSVBQREISIARKPLVA 220
 PVKMPGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPVVA 221
91.2%; Score 1156; DB 5; 96.4%; Pred. No. 1.7e-116; iive 3; Mismatches 5;
 Search completed: August 12, 2004, 06:17:05 Job time: 88.5717 secs
 Best Local Similarity 96.4
Matches 212; Conservative
 61
 62
 121
 Query Match
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

August 12, 2004, 06:12:47; Search time 6.44467 Seconds (without alignments) 745.314 Million cell updates/sec

US-09-890-463-2 83

1 SVIAKOMTYKVYMSGTV 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:\*

1. geneseqp1980s:\*
2. geneseqp200s:\*
4. geneseqp200s:\*
5. geneseqp2001s:\*
6. geneseqp2003as:\*
7. geneseqp2003as:\*
8. geneseqp2003bs:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

|           | Description    |          |          | Pigment  | _        |          | Abp69957 Colour Fa |          | Abp69952 Colour Fa | Abp69925 Colour Fa | Abp69947 Colour Fa |          |          |          | Abp69955 Colour Fa | _        |          | Abp69958 Colour Fa | Colour F | Abp69953 Colour Fa |          | Colour   | 127      | Colour   | Abp69926 Colour Fa | Abp69956 Colour Fa |
|-----------|----------------|----------|----------|----------|----------|----------|--------------------|----------|--------------------|--------------------|--------------------|----------|----------|----------|--------------------|----------|----------|--------------------|----------|--------------------|----------|----------|----------|----------|--------------------|--------------------|
| SUMMAKIES | ΙD             | AAY97148 | AAY97151 | AAY97152 | ABP69949 | ABP69944 | ABP69957           | ABP69941 | ABP69952           | ABP69925           | ABP69947           | ABP69959 | ABP69940 | ABP69943 | ABP69955           | ABP69929 | ABP69934 | ABP69958           | ABP69939 | ABP69953           | ABP69938 | ABP69945 | ABP69927 | ABP69946 | ABP69926           | ABP69956           |
|           | DB             |          | m        | m        | ß        | Ŋ        |                    |          |                    |                    |                    |          |          |          |                    |          | ა        |                    |          |                    |          |          | Ŋ        |          | Ŋ                  | ហ                  |
|           | Length         | 17       | 18       | 25       | 169      | 169      | 200                | 220      | 220                | 220                | 220                | 220      | 220      | 220      | 220                | 220      | 220      | 220                | 220      | 220                | 220      | 220      | 220      | 220      | 220                | 220                |
| <b>-}</b> | Query<br>Match | 0        | 100.0    | 100.0    | 100.0    | 100.0    | 100.0              | 100.0    | 100.0              | 100.0              | 100.0              | 100.0    | 100.0    | 100.0    | 100.0              | 100.0    | 100.0    | 100.0              | 100.0    | 100.0              | 100.0    | 100.0    | 100.0    |          | 100.0              | 100.0              |
|           | Score          | 83       | 83       | 83       | 83       | 83       | 83                 | 83       | 83                 | 83                 | 83                 | 83       | 83       | 83       | 83                 | 83       | 83       | 83                 | 83       | 83                 | 83       | . 83     | 83       | 83       | 83                 | 83                 |
|           | Result<br>No.  |          | 2        | m        | 4        | 2        |                    | 7        | 80                 | 6                  | 10                 | 11       | 12       | 13       | 14                 | 15       | 16       | 17                 | 18       | 19                 | 20       | 21       | 22       | 23       |                    | 25                 |

| 220 5 ABP69937 220 5 ABP69932 220 5 ABP69932 220 5 ABP69931 220 5 ABP69936 220 5 ABP69936 220 5 ABP69930 222 5 ABP70023 222 5 ABP70023 223 5 ABP70033 223 5 ABP70033 223 5 ABP70033 223 5 ABP70033 223 5 ABP70034 223 5 ABP70035 223 5 ABP70036 231 5 ABP70025 | Abp69937 COLOUR FA Abp69932 COLOUR FA Abp69928 COLOUR FA Abp69935 COLOUR FA Abp69948 COLOUR FA Abp69948 COLOUR FA Abp70037 COLOUR FA Abp70033 COLOUR FA Abp70032 COLOUR FA Abp70032 COLOUR FA | Abp70036 Colour Fa<br>Aay97149 Pigment p | Colour F<br>Pigment  |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------|----------------------|
|                                                                                                                                                                                                                                                                                                                                                                                                       | ABP69937 ABP69932 ABP69931 ABP69931 ABP69935 ABP69948 ABP70037 ABP70027 ABP70027 ABP70027 ABP70027 ABP70027 ABP70027 ABP70033 ABP70030                                                                                                                                                                                                                                                                         | ABP70036<br>AAY97149                     | ABP70025<br>AAY97150 |
|                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                                                                                                                                                                                                                                                                                                                |                                          | 3 2                  |
|                                                                                                                                                                                                                                                                                                                                                                                                       | 1000.0<br>1000.0<br>1000.0<br>1000.0<br>1000.0<br>1000.0<br>1000.0                                                                                                                                                                                                                                                                                                                                             | 100.0                                    | 100.0                |
| 10000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                                                                | 83                                       | 83                   |
|                                                                                                                                                                                                                                                                                                                                                                                                       | 22222222222224422222444522222244452452445244524452445445                                                                                                                                                                                                                                                                                                                                                       | 42                                       | 44                   |

## ALIGNMENTS

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The N-terminal peptides shown in AAV97147-48 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to clollow gene expression in transformed tissues) or general dyestuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters
 Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 N-terminal; pigment protein from coral tissue; PPCT; fluorescence; tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet; UV filter.
 Pigment protein from coral tissue N-terminal peptide 2.
 AAY97148 standard; peptide; 17 AA
 Claim 4; Page 42; 49pp; English.
 02-FEB-2000; 2000WO-AU000056.
 99AU-00008463
 Hoegh-Guldberg O, Dove S;
 (first entry)
 WPI; 2000-532892/48.
 (UNSY) UNIV SYDNEY.
 Acropora horrida.
 WO200046233-A1.
 02-FEB-1999;
 04-DEC-2000
 10-AUG-2000.
 AAY97148;
RESULT 1
```

Sequence 17 AA;

Query Match

100.0%; Score 83; DB 3; Length 17;

a

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12-SEP-2002
 ABP69949;
 ABP69949

IID ABP6

AC ABP6

XX

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C2-J

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DD COLC

KW Chrc

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 RESULT 4
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 The N-terminal peptides shown in AAY97151-52 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, increscent marker (e.g. to follow gene expression in transformed tissues) or general dyscutf (all claimed). PPCT may also be used in sunscreen formulations or UV filters
 Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 N-terminal; pigment protein from coral tissue; PPCT; fluorescence;
tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet;
UV filter.
 Gaps
 Gaps
 ..
0
 .,
 Length 18;
 0; Indels
 Indels
 Pigment protein from coral tissue N-terminal peptide 3.
 0
 Score 83; DB 3; I
Pred. No. 3.8e-08;
100.0%; Pred. No. 3.6e-08;
 Mismatches
 Mismatches
 ¥.
 AAY97152 standard; peptide; 25 AA.
 Example 2; Page 18; 49pp; English
 100.0%; Sc
100.0%; Pr
tive 0;
 .
0
 AAY97151 standard; peptide; 18
 1 SVIAKQMTYKVYMSGTV 17
 1 SVIAKOMTYKVYMSGTV 17
 1 SVIAKOMTYKVYMSGTV 17
 SVIAKOMTYKVYMSGTV 17
 02-FEB-2000; 2000WO-AU000056.
 99AU-00008463.
 Dove S;
 (first entry)
 (first entry)
 Query Match
Best Local Similarity 100.
Matches 17; Conservative
 17; Conservative
 Acropora aspera.
Montipora caliculata.
 WPI; 2000-532892/48.
 Porites murrayensis.
 (UNSY) UNIV SYDNEY
Best Local Similarity
 Hoegh-Guldberg O,
 Sequence 18 AA;
 WO200046233-A1
 (both claimed)
 02-FEB-1999;
 04-DEC-2000
 04-DEC-2000
 10-AUG-2000
 AAY97151;
 AAY97152;
 Matches
 RESULT 3
 RESULT 2
 AAY97152
 g
 1 X X X X X A
 à
 à
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The N-terminal peptides shown in AAY97151-52 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700
 Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dyestuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters (both claimed)
 N-terminal; pigment protein from coral tissue; PPCT; fluorescence; tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet;
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; detromophore; blomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen.
 .
0
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 70.
 Length 25;
 0; Indels
Pigment protein from coral tissue N-terminal peptide 4.
 Score 83; DB 3; I
Pred. No. 5.6e-08;
; Mismatches 0;
 ABP69949 standard; protein; 169 AA.
 Example 2; Page 18; 49pp; English
 .;
0
 100.0%;
 1 SVIAKOMIYKVYMSGIV 17
 SVIAKOMTYKVYMSGTV 17
 01-MAR-2002; 2002WO-GB000928.
 02-MAR-2001; 2001US-0273227P.
 02-FEB-2000; 2000WO-AU000056.
 99AU-00008463
 Dove S;
 (first entry)
 17; Conservative
 WPI; 2000-532892/48.
 (UNSY) UNIV SYDNEY
 Query Match
Best Local Similarity
Matches 17; Conserv
 Hoegh-Guldberg O,
 Sequence 25 AA;
 Porites lobata.
 WO200046233-A1.
 WO200270703-A2
 02-FEB-1999;
 22-JAN-2003
 Platygyra sp
 10-AUG-2000.
```

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Dove SG;

Mason J,

```
The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other extracts, e.g. flavouring, beverage or juice or colouring agent. Other cuses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car conting materials that experience UV damage e.g. plastics and car conting materials that experience UV damage e.g. plastics and car conting materials plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketablity. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 Colour facilitating molecule; CFM; green fluorescent protein, GFP, chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 60.
 100.0%; Score 83; DB 5; Length 169; 100.0%; Pred. No. 5.2e-07; tive 0; Mismatches 0; Indels
 ABP69944 standard; protein; 169 AA.
 Brugliera F,
 Claim 5; Page 349; 510pp; English.
 Prescott M;
 1 SVIAKOMTYKVYMSGTV 17
 1 SVIAKOMTYKVYMSGTV 17
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 (first entry)
 17; Conservative
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Porites murrayensis.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80
 Best Local Similarity
 UV sink; sunscreen
 (JONE/) JONES E L.
 Sequence 169 AA;
 WO200270703-A2.
 22-JAN-2003
 12-SEP-2002
 white light
 ABP69944;
 Query Match
 Matches
 RESULT 5
ABP69944
 à
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for cotaling materials that experience UV damage e.g. place and/or corals, for upholstery. CFMs are useful in the flower industry, in the development of many varieties of flowering plants. Other contemplated uses include,
 expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen.
 Colour facilitating molecule; CFM; green fluorescent protein; GFP;
 ;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 84.
 Length 169;
 0; Indels
 Dove SG;
 100.0%; Score 83; DB 5; I 100.0%; Pred. No. 5.2e-07; ative 0; Mismatches 0;
 Brugliera F, Mason J,
Prescott M:
 ABP69957 standard; protein; 200 AA.
 Claim 5; Page 337; 510pp; English.
 1 SVIAKOMTYKVYMSGTV 17
 1 SVIAKOMTYKVYMSGTV 17
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
01-MAR-2002; 2002WO-GB000928.
 02-MAR-2001; 2001US-0273227P.
 (revised)
(first entry)
 17; Conservative
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80
 Local Similarity
 (UYQU) UNIV QUEEN
(JONE/) JONES E L.
 Sequence 169 AA;
 acid sequences
 Montipora sp
 white light.
 06-AUG-2003
22-JAN-2003
 ABP69957;
 Query Match
 Matches
 RESULT 6
 ABP6995'
g
 .;
0
 Gaps
 0;
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Millepora sp.

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The invention relates to an isolated colour-facilitating molecule (CFM)

comprising a polypeptide which, in a cell, alone or together with one or

come other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

conventioned fleece. They are useful for producing only extraneous

concloured fleece. They are useful for producing ocloured plant

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

consting materials that experience UV damage e.g. plastics and car

conting materials that experience UV damage e.g. plastics and car

cupholstery. CFMs are useful in the flower industry, in the development of

me varieties of flowering plants. Other contemplated uses include,

conting markers, general reporter molecules, photon traps, UV sinks or

conting markers, general reporter molecules, photon traps, UV sinks or

conting species, and in fruits and vegetables to enhance their

conting marketablity. CFMs embedded in a gel matrix improve image quality in

conting marketablic and in the colour in edible and/or ornamental

conting marketablic and in the colour in mineroremance their

conting marketablic and in the colour in mineroremance their

conting marketablic and in the colour in market and colour in a gel market and colour in market
 0
 marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP5024-ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.)
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule, CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen.
 0;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 54.
 / match
Local Similarity 100.0%; Score 83; DB 5; Length 200;
les 17; Conservative 0; Mismatcher.
 Karan M, Brugliera F, Mason J, Dove SG;
 Claim 5; Page 363-364; 510pp; English.
 ABP69941 standard; protein; 220 AA.
 Prescott M;
 1 SVIAKOMTYKVYMSGTV 17
 1 SVIAKOMTYKVYMSGTV 17
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 2001US-0273227P
 01-MAR-2002; 2002WO-GB000928
 (first entry)
 UNIV QUEENSLAND.
 WPI; 2002-740765/80
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 (NUFA-) NUFARM LID
 (UYQU) UNIV QUEEN!
(JONE/) JONES E L.
 Sequence 200 AA;
WO200270703-A2
 22-JAN-2003
 white light.
 12-SEP-2002
 ABP69941;
 Query Match
 Matches
 RESULT 7
 ABP69941
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human ey in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a cransgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other cases include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs embedded in a gel matrix improve image quality in altuations of distorted light specira (homatrix). The first all-protein altuations of distorted light specira.
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 74.
 ;
0
 100.0%; Score 83; DB 5; Length 220; 100.0%; Pred. No. 7e-07; ive 0; Mismatches 0; Indels
 Dove SG;
 Mason J,
 Claim 5; Page 330-331; 510pp; English.
 ABP69952 standard; protein; 220 AA.
 Brugliera F,
Prescott M;
 100.08; FIL
 17
 1 SVIAKOMTYKVYMSGTV 17
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928.
 1 SVIAKOMTYKVYMSGTV
 22-JAN-2003 (first entry)
 17; Conservative
 UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 Query Match
Best Local Similarity
 (NUFA-) NUFARM LTD
 Hoegh-Guldberg IO,
 (UYQU) UNIV QUEEN.
(JONE/) JONES E L.
 Sequence 220 AA;
 WO200270703-A2
 acid sequences
 12-SEP-2002.
 white light.
 Jones EL,
 ABP69952;
 RESULT 8
 ABP69952
 XXXXXXXXX
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Comprising a polypeptide which, in a cell, alone or together with one or comprising a polypeptide which, in a cell, alone or together with one or core ther molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a cranspanic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing ocloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other cuses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower indusery, in the development of composition markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs and in fruits and vegetables to enhance their commental cfungal species, and in fruits and vegetables to enhance their commental committee their committees of fungal species, and in fruits and vegetables to enhance their committees of their correct contemplate image quality in the marketability. CFMs embedded in a gel matrix improve image quality in the contemplate and cont
 marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorecent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
chromophore, biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap; UV sink; sunscreen.
 Score 83; DB 5; Length 220; Pred. No. 7e-07;
 Dove SG;
 Mason J,
 Mismatches
 Claim 5; Page 351-352; 510pp; English.
 ABP69925 standard; protein; 220 AA.
 Brugliera F,
 0;
 Prescott M;
 100.0%;
 1 SVIAKOMTYKVYMSGTV 17
 1 SVIAKOMTYKVYMSGTV 17
 01-MAR-2002; 2002WO-GB000928.
 2001US-0273227P.
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 (first entry)
 Local Similarity 100.
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 Hoegh-Guldberg IO,
 JONES E L.
 Sequence 220 AA;
 WO200270703-A2
 22-JAN-2003
 Platygyra sp.
 02-MAR-2001;
 21-MAR-2001;
 12-SEP-2002
 white light
 ABP69925;
 Jones EL,
 Query Match
 (JONE/)
 Best Loca
Matches
 RESULT 9
 ABP69925
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleace. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for cocating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include,
 or
 expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 0;
Colour Facilitating molecule (CFM) related sequence #SEQ ID 22
 100.0%; Score 83; DB 5; Length 220; 100.0%; Pred. No. 7e-07; ive 0; Mismatches 0; Indels
 Dove SG;
 Brugliera F, Mason J,
 Claim 5; Page 286-287; 510pp; English.
 ABP69947 standard; protein; 220 AA.
 Prescott M;
 17
 1 SVIAKOMTÝKVYMSGTV 17
 01-MAR-2002; 2002WO-GB000928
 02-MAR-2001; 2001US-0273227P
 21-MAR-2001; 2001AU-00003874
15-OCT-2001; 2001US-0329816P
 1 SVIAKOMTYKVYMSGTV
 Local Similarity 100.
es 17; Conservative
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
(JONE/) JONES E L.
 Karan M,
 WPI; 2002-740765/80
 Hoegh-Guldberg IO,
 UV sink; sunscreen
 Sequence 220 AA;
 Acropora aspera.
 WO200270703-A2.
 white light.
 12-SEP-2002
 Jones EL,
 Query Match
 RESULT 10
ABP69947
ID ABP69
XX
AC ABP69
 Matches
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Gaps

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0; Indels

ABP69947;

Colour facilitating molecule, CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;

UV sink; sunscreen

WO200270703-A2.

12-SEP-2002.

Montipora sp

Colour Facilitating molecule (CFM) related sequence #SEQ ID 88.

(first entry)

22-JAN-2003

06-AUG-2003 ABP69959;

(revised)

ABP69959 standard; protein; 220 AA.

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The invention relates to an isolated colour-facilitating molecule (CFW)

Comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

transgenic animal which exhibits a novel colour e.g. sheep with blue or

coloured fleece. They are useful for producing coloured plant

contacts, e.g. flavouring, beverage or juice or colouring agent. Other

cuses include transducing or intensifying an image, providing additional

clight for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics

coating additional

coating additiona
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 Colour facilitating molecule, CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 66.
 Karan M, Brugliera F, Mason J, Dove SG;
 Claim 5; Page 344-345; 510pp; English.
 Prescott M;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 (first entry)
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 WPI; 2002-740765/80.
 Hoegh-Guldberg IO,
 UV sink; sunscreen
 (UYQU) UNIV QUEEN
(JONE/) JONES E L.
 Sequence 220 AA;
 WO200270703-A2
 acid sequences
 Platygyra sp.
 white light.
 12-SEP-2002.
22-JAN-2003
 Jones EL,
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Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-

Brugliera F, Mason J, Dove SG;

Prescott M;

Karan M,

WPI; 2002-740765/80. Jones EL, Karan M, Hoegh-Guldberg IO,

white light.

02-MAR-2001; 2001US-0273227P. 21-MAR-2001; 2001AU-00003874. 15-OCT-2001; 2001US-0329816P.

(UYQU ) UNIV QUEENSLAND. (JONE/) JONES E L.

(NUFA-) NUFARM LTD. (UYQU ) UNIV QUEENS

01-MAR-2002; 2002WO-GB000928.

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The invention relates to an isolated colour-facilitating molecule (CFM) more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of many varieties of flowering plants. Other contemplated uses include.
 expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABS6924-ABP70048 represent CFM related amino acid sequences. (Updated on 06-AUG-2003 to correct OS field.)
 Gaps
 .
0
 100.0%; Score 83; DB 5; Length 220; 100.0%; Pred. No. 7e-07; ive 0; Mismatches 0; Indels
 Claim 5; Page 368-369; 510pp; English.
 1 SVIAKOMTYKVYMSGTV 17
 17; Conservative
 Best Local Similarity
 Sequence 220 AA;
 Query Match
 Matches
ò
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SVIAKOMTYKVYMSGTV 17 g

. 0

Gaps

0;

100.0%; Score 83; DB 5; Length 220; 100.0%; Pred. No. 7e-07; cive 0; Mismatches 0; Indels

1 SVIAKOMIYKVYMSGTV 17 SVIAKOMTYKVYMSGTV 17

Local Similarity 100.

Matches

à

Query Match

· 0

RESULT 11 ABP69959

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The invention relates to an isolated colour-facilitating molecule (CFM)

Comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

cransgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing coloured plant

extracts, e.g. flavouring, beverage or juice or colouring agent. Other

cuses include transducing or intensifying an image, providing additional

light for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

upholstery. CFMs are useful in the flower industry, in the development of

new varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs endedded in a gel matrix improve image quality in

cmarketability. CFMs embedded in a gel matrix improve image quality in

characters of the contemplate photoric in the first all-protein
 chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino acid sequences
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 52.
 Claim 5; Page 327-328; 510pp; English.
 ABP69940 standard; protein; 220 AA.
 Brugliera F,
 Prescott M;
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928.
 (first entry)
 UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 JV sink; sunscreen.
 (NUFA-) NUFARM LID
 (JONE/) JONES E L.
 Hoegh-Guldberg IO,
 Sequence 220 AA;
 WO200270703-A2.
 Millepora sp.
 22-JAN-2003
 12-SEP-2002,
 white light
 ABP69940;
 Jones EL,
 UYQU
RESULT 12
 ABP69940
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Dove SG;

Mason J,

```
The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human ey in the absence of excitation by extraneous on-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant care useful for producing ocloured plant care uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for the coating materials that experience UV damage e.g. plactic and care upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs endify visible colour in edible and/or ornamental chungal species, and in fruits and vegetables to enhance thair all propersion markets all and plants. Other contemplated uses include, marketablity. CFMs embodded in a gel marrix improve image quality in marketablity. The marrix improve image quality in marketablity.
 situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The sequences given in records ABP69924-ABP70048 represent CFM related amino
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 chromophore; biomatrix; transgenic animal; colouring agent;
flower industry; expression marker; reporter molecule; photon trap;
 Colour facilitating molecule; CFM; green fluorescent protein; GFP;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID
 Mason J, Dove SG;
 Brugliera F,
 Claim 5; Page 335; 510pp; English.
 ABP69943 standard; protein; 220
 Prescott M;
17
 17
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928.
 1 SVIAKOMTYKVYMSGTV
 (first entry)
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Karan M,
 Porites murrayensis.
 WPI; 2002-740765/80
 flower industry; ex
UV sink; sunscreen.
 Hoegh-Guldberg IO,
 (JONE/) JONES E L.
 WO200270703-A2
 22-JAN-2003
 white light
 12-SEP-2002
 ABP69943;
 Jones EL,
 RESULT 13
 ABP69943
```

100.0%; Score 83; DB 5; Length 220;

Sequence 220 AA;

Query Match

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Gaps

0;

100.0%; Score 83; DB 5; Length 220; 100.0%; Pred. No. 7e-07; ive 0; Mismatches 0; Indels

100.0%; Pred.

Query Match
Best Local Similarity 100.
Matches 17; Conservative

α

us-09-890-463-2.rag

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à

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The invention relates to an isolated colour-facilitating molecule (CFW)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

con-white light or particle emission. CFMs are useful for producing a

cransgenic animal which exhibits a novel colour e.g. sheep with blue or

red coloured fleece. They are useful for producing ocloured plant

catracts, e.g. flavouring, beverage or juice or colouring agent. Other

catracts, e.g. flavouring, beverage or juice or colouring agent. Other

catracts and car

catracts and car

light for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience W damage e.g. plastics and car

coating materials that experience worleanly, in the development of

new varieties of flowering plants. Other contemplated uses include,

expression markers, general reporter molecules, photon traps, UV sinks or

in sunscreens. CFMs embedded in a gel matrix improve image quality in

changed species, and in fruits and vegetables to enhance their

chromophore to be isolated was Green Fluorescent protein (GFP). The

sequences given in records ABREGGB24-ABP710048 represent CFM related amino

acid sequences: (Updated on 06-AUG-2003 to correct OS field.)
 ó
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule, CFM; green fluorescent protein, GFP, chromophore, biomatrix, transgenic animal, colouring agent, flower industry, expression marker, reporter molecule, photon trap,
 .;
0
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 80.
 7e-07;
ra 0; Indels
 Dove SG;
 Mason J,
100.0%; Pred. ...
 ABP69955 standard; protein; 220 AA.
 Karan M, Brugliera F,
 Claim 5; Page 359; 510pp; English.
 Prescott M;
 1 SVIAKOMTYKVYMSGTV 17
 SVIAKOMTYKVYMSGTV 17
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 (first entry)
 17; Conservative
 UNIV QUEENSLAND.
 (revised)
 WPI; 2002-740765/80
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 UV sink; sunscreen.
 Best Local Similarity
 (NUFA-) NUFARM LTD
 (UYQU) UNIV QUEEN!
 Pavona decussata.
 WO200270703-A2
 06-AUG-2003
22-JAN-2003
 12-SEP-2002,
 white light.
 ABP69955;
 Matches
 ABP69955
```

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The invention relates to an isolated colour-facilitating molecule (CFW) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous con-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing ocloured fleece. They are useful for producing ocloured plant cases include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for uses include transducing or intensifying an inage, providing additional light for growing phototropic organisms e.g. algae and/or corals, for upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, cay resision markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in
 .
0
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule, CFM, green fluorescent protein, GFP, chromophore, biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 ;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 30.
 Length 220;
 Score 83; DB 5; Length 22.
Pred. No. 7e-07;
 Dove SG;
 Brugliera F, Mason J,
Prescott M;
 Claim 5; Page 296-297; 510pp; English.
 ABP69929 standard; protein; 220 AA.
 100.0%; Sc
100.0%; Pr
tive 0;
 17
 17
 01-MAR-2002; 2002WO-GB000928,
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 1 SVIAKOMTYKVYMSGTV
 1 SVIAKOMTYKVYMSGTV
 (first entry)
 17; Conservative
 (NUFA-) NUFARM LID.
(UYQU) UNIV QUEENSLAND.
(JONE/) JONES E L.
 chromophore, biomatrix;
 (revised)
 Karan M,
 WPI; 2002-740765/80.
 Query Match
Best Local Similarity
 Hoegh-Guldberg IO,
 UV sink; sunscreen
Sequence 220 AA;
 Acanthastrea sp.
 WO200270703-A2.
 12-SEP-2002.
 06-AUG-2003
 22-JAN-2003
 white light
 ABP69929;
 Colour
 Matches
 Jones
 RESULT 15
 ABP69929
ID ABP6
XX
 g
 à
```

CC situations of distorted light spectra (biomatrix). The first all-protein CC chromophore to be isolated was Green Fluorescent protein (GFP). The CC sequences given in records ABP69924-ABP70048 represent CFM related amino CC acid sequences. (Updated on 06-AUG-2003 to correct OS field.)

XX

Query Match

Query Match

Best Local Similarity 100.0%; Score 83; DB 5; Length 220;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: August 12, 2004, 06:17:04 Job time : 6.44467 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 12, 2004, 06:12:47 ; Search time 1.89549 Seconds (without alignments) 745.314 Million cell updates/sec

US-09-890-463-1 21 1 SVIAK 5

Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\* geneseqp1980s:\* geneseqp1990s:\* ٠, Database

geneseqp2003bs:\* geneseqp2004s:\* geneseqp2003as:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| 179VEA | AAY97147 | m  | Ŋ      | 100.0        | 21        | н      |
|--------|----------|----|--------|--------------|-----------|--------|
|        |          | 1  |        |              | 1 1 1 1 1 |        |
| Descri | Π        | DB | Length | Match        | Scor      | No.    |
|        |          |    |        | Query        |           | Result |
|        |          |    |        | o <b>j</b> e |           |        |

|            | Description | Aay97147 Pigment D | Abb99061 N-termina |          | ۵        |          |          | Abb99074 N-termina |          | Aay97148 Pigment p | 1 Pigment | 2 Pigment | 2 C-myb pr | Novel    | 9 Human  | 3 N. don | 2 Hum    | 3 Novel  | Novel    | Abp39391 Staphyloc | 64       | Novel    | Human    | 2 Human  | 4 Human  | 4 Human  |
|------------|-------------|--------------------|--------------------|----------|----------|----------|----------|--------------------|----------|--------------------|-----------|-----------|------------|----------|----------|----------|----------|----------|----------|--------------------|----------|----------|----------|----------|----------|----------|
| SUMMARIES  | ID          | AAY97147           | ABB99061           | AAG87969 | AAG87968 | ABP70008 | ABB99073 | ABB99074           | ABB99072 | AAY97148           | AAY97151  | AAY97152  | AAB62002   | ABG14062 | ABP34419 | ABP77483 | ABB12172 | ABG16073 | ABG16074 | ABP39391           | AAG01464 | ABG16071 | AAY29549 | AAB44472 | AAE13814 | ADD66504 |
|            | DB          | m                  | 2                  | 4        | 4        | 2        | S        | Ŋ                  | 2        | m                  | m         | ٣         | 4          | 4        | Ŋ        | 9        | 4        | 4        | 4        | S                  | ო        | 4        | 7        | m        | 4        | 7        |
|            | Length      | IJ                 | Ŋ                  | 10       | 10       | 13       | 16       | 16                 | 16       | 17                 | 18        | 25        | 20         | 73       | 73       | 75       | 16       | 16       | 78       | 81                 | 89       | 91       | 102      | 102      | 102      | 102      |
| *<br>Query | Match       | 100.0              | 100.0              | 100.0    | 100.0    | 100.0    | 100.0    | 100.0              | 100.0    | 100.0              | 100.0     | 100.0     | 100.0      | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    | 100.0    |                    | 100.0    |          | 100.0    | 100.0    | ö        | 100.0    |
|            | Score       | 21                 | 21                 | 21       | 21       | 21       | 21       | 21                 | 21       | 21                 | 21        | 21        | 21         | 21       | 21       | 21       | 21       | 21       | 21       | 21                 | 21       | 21       | 21       | 21       | 21       | 21       |
| Result     | No.         | н                  | 7                  | ĸ        | 4        | Ŋ        | 9        | 7                  | 80       | Ø.                 | 10        | 11        | 12         | 13       | 14       | 15       | 16       | 17       |          | 19                 | 20       | 21       | 22       | 23       | 24       | 25       |

| Ade87758 Human lun | Adc95761 E. faeciu | Abm70003 Photorhab | Abg16072 Novel hum | Abg14060 Novel hum | Human    |          | Abp69949 Colour Fa | Abp69944 Colour Fa | Abg03673 Novel hum | Novel    | Staph    | Abp65304 Bifidobac | Abp69957 Colour Fa | Abb47893 Listeria | Abp69941 Colour Fa | Abp69952 Colour Fa | Colour   | Colour   | Abp69947 Colour Fa |
|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|-------------------|--------------------|--------------------|----------|----------|--------------------|
| ADE87758           | ADC95761           | ABM70003           | ABG16072           | ABG14060           | ABP08878 | ABM69564 | ABP69949           | ABP69944           | ABG03673           | ABG07747 | ABM73297 | ABP65304           | ABP69957           | ABB47893          | ABP69941           | ABP69952           | ABP69925 | ABP69954 | ABP69947           |
| 7                  | 7                  | 9                  | 4                  | 4                  | Ŋ        | 9        | Ŋ                  | Ŋ                  | 4                  | 4        | 9        | Ŋ                  | ъ                  | 5                 | 2                  | 2                  | Ŋ        | Ŋ        | Ŋ                  |
| 102                | 111                | 137                | 144                | 144                | 147      | 158      | 169                | 169                | 180                | 182      | 188      | 196                | 200                | 200               | 220                | 220                | 220      | 220      | 220                |
| 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0    | 100.0    | 100.0              | 100.0              | 100.0              | 100.0    | 100.0    | 100.0              | 100.0              | 100.0             | 100.0              | 100.0              | 100.0    | 100.0    | 100.0              |
| 21                 | 21                 | 21                 | 21                 | 21                 | 21       | 21       | 21                 | 21                 | 21                 | 21       | 21       | 21                 | 21                 | 21                | 21                 | 21                 | 21       | 21       | 21                 |
| 26                 | 27                 | 28                 | 29                 | 30                 | 31       | 32       | 33                 | 34                 | 35                 | 36       | 37       | 38                 | 39                 | 40                | 41                 | 42                 | 43       | 44       | 45                 |

## ALIGNMENTS

AAY97147 standard; peptide; 5 AA. RESULT 1 AAY97147

AAY97147;

Pigment protein from coral tissue N-terminal peptide 1.

(first entry)

04-DEC-2000

N-terminal, pigment protein from coral tissue, PPCT, fluorescence; tissue marker, fluorescent marker; dyestuff; sunscreen; ultra violet; UV filter.

Acropora aspera.
Acropora horrida.
Montipora caliculata.
Montipora monasteriata. 

Porites murrayensis. Porites lobata.

WO200046233-A1. 10-AUG-2000.

02-FEB-2000; 2000WO-AU000056. 99AU-00008463 02-FEB-1999;

Hoegh-Guldberg O, Dove S; (UNSY ) UNIV SYDNEY.

WPI; 2000-532892/48.

Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.

Claim 3; Page 42; 49pp; English.

The N-terminal peptides shown in AAY97147-48 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dysetuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters

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$ X C C C C C
 The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell more other usualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or ed coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional collish for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their
 ö
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 0;
 Score 21; DB 3; Length 5, Pred. No. 1.4e+06;
 Dove SG;
 Mason J,
 N-terminal amino acid sequence of a CFM #1
 Brugliera F,
 Claim 3; Page 278; 510pp; English.
 ABB99061 standard; peptide; 5 AA
 0;
 Prescott M;
 100.0%;
 2001US-0273227P.
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 (first entry)
 Conservative
 (UYQU) UNIV QUEENSLAND.
(JONE/) JONES E L.
 Karan M,
 WPI; 2002-740765/80
 Similarity
5; Conserva
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 (NUFA-) NUFARM LID.
 sink; sunscreen
 2
 ເນ
 SVIAK
 1 SVIAK
 WO200270703-A2
 Sequence 5 AA;
 (both claimed)
 Unidentified
 02-MAR-2001;
 22-JAN-2003
 white light.
 12-SEP-2002
 ABB99061;
 Query Match
Best Local
 Matches
 RESULT 2
 ABB9906:
 g
 SSXC
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0
 0;
 The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
situations of distorted light spectra (biomatrix). The first all-protein chromophore to be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a colour-facilitating molecule (CFM)
 Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design.
 Saccharomyces cerevisiae; complementary peptide; peptide identification;
 Gaps
 Gaps
 ..
 ·.
 Similarity 100.0%; Score 21; DB 4; Length 10; Similarity 100.0%; Pred. No. 25; Conservative 0; Mismatches 0; Indels
 100.0%; Score 21; DB 5; Length 5; 100.0%; Pred. No. 1.4e+06;
 Indels
 Saccharomyces cerevisiae peptide, SEQ ID NO: 2918.
 0;
 Mismatches
 Example 5; Page 432; 488pp; English
 AAG87968 standard; peptide; 10 AA.
 AAG87969 standard; peptide; 10 AA
 0;
 13-DEC-2000; 2000WO-GB004773.
 99GB-00029471.
 drug discovery, drug design.
 (first entry)
 Saccharomyces cerevisiae.
 Saccharomyces cerevisiae
 Conservative
 Roberts GW, Heal JR;
 (PROT-) PROTEOM LID.
 WPI; 2001-367863/38.
 Query Match
Best Local Similarity
Matches 5; Conserv
 Query Match
Best Local Similarity
Matches 5; Conserv
 10
 Ŋ
 1 SVIAK 5
 Ŋ
 Sequence 10 AA;
 SVIAK
 SVIAK
 WO200142276-A1.
 SVIAK
 Sequence 5 AA;
 13-DEC-1999;
 11-SEP-2001
 14-JUN-2001
 AAG87969;
 RESULT 4
AAG87968
ID AAG8
 RESULT 3
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Page

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The invention relates to the identification of complementary peptides by analysis of protein and nucleotide sequence databases from higher eukaryotic genomes, excluding human and plants. The specific complementary peptides interact with their relevant target proteins encoded in the eukaryote genome. The peptides may be used as reagents and drugs for drug discovery and as lead ligands for drug design and development. The present sequence is a complementary peptide from
 Identifying complementary peptides by analysis of protein and nucleotide sequence databases, useful in drug design.
 cerevisiae; complementary peptide; peptide identification;
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 Colour Facilitating molecule (CFM) related sequence #SEQ ID 184.
 100.0%; Score 21; DB 4; Length 10; 100.0%; Pred. No. 25; o; Mismatches 0; Indels
 Saccharomyces cerevisiae peptide, SEQ ID NO: 2917.
 Example 5; Page 432; 488pp; English.
 ABP70008 standard; peptide; 13 AA.
 13-DEC-2000; 2000WO-GB004773.
 99GB-00029471.
 drug discovery; drug design
 (first entry)
 (first entry)
 Saccharomyces cerevisiae.
 5; Conservative
 Saccharomyces cerevisiae
 (revised)
 Heal JR;
 (PROT-) PROTEOM LID.
 WPI; 2001-367863/38
 Best Local Similarity
 UV sink; sunscreen
 SVIAK 10
 1 SVIAK 5
 Pavona decussata.
 Sequence 10 AA;
 40200270703-A2
 WO200142276-A1
 13-DEC-1999;
 Roberts GW,
 06-AUG-2003
22-JAN-2003
 12-SEP-2002.
 14-JUN-2001
 AAG87968;
 ABP70008;
 Query Match
 Matches
 ABP70008
```

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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their all-protein chromophore to be isolated and segmental chromophore to be isolated and segmental chromophore given in records ABPST90048 represent CFM sequence in records ABPST90048 represent content of mains and or the content of the content of the chromophore of the content of the content of the content of the content of the chromophore of the content of the con
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule; CFM; green fluorescent protein; GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 .:0
 acid sequences. (Updated on 06-AUG-2003 to correct OS field.
 100.0%; Score 21; DB 5; Length 13; 100.0%; Pred. No. 33; trive 0; Mismatches 0; Indels
 Dove SG
 N-terminal amino acid sequence of a CFM #13.
 Mason J,
 Brugliera F,
Prescott M;
 Claim 5; Page 473; 510pp; English.
 ABB99073 standard; peptide; 16 AA.
01-MAR-2002; 2002WO-GB000928.
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 2001US-0273227P
 (first entry)
 Conservative
 UNIV QUEENSLAND
 Query Match
Best Local Similarity
5; Conserv?
 Karan M,
 WPI; 2002-740765/80.
 flower industry; ex
UV sink; sunscreen.
 (NUFA-) NUFARM LTD
 Jones EL, Karan M.
Hoegh-Guldberg IO,
 (UYQU) UNIV QUEEN: (JONE/) JONES E L.
 Sequence 13 AA;
 1 SVIAK
 1 SVIAK
 WO200270703-A2
 02-MAR-2001;
 Unidentified
 white light.
 22-JAN-2003
 ABB99073;
 RESULT 6
 ABB99073
 d
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Gaps

.

0

Unidentified

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The invention relates to an isolated colour-facilitating molecule (CFW)

comprising a polypeptide which, in a cell, alone or together with one or

more other molecules imparts an altered visual characteristic to the cell

when visualised by a human eye in the absence of excitation by extraneous

non-white light or particle emission. CFMs are useful for producing a

cranspenic animal which exhibits a novel colour e.g. sheep with blue or

cranspenic animal winch exhibits a novel colour e.g. sheep with blue or

cranspenic animal winch exhibits a novel colour e.g. sheep with blue or

cranscription of the stransducing or intensifying an image, providing additional

clight for growing phototropic organisms e.g. algae and/or corals, for

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics and car

coating materials that experience UV damage e.g. plastics and car

conting materials that experience UV damage e.g. plastics and car

conting materials that experience UV damage e.g. plastics and car

conting materials that experience UV damage e.g. plastics and car

conting materials that experience UV damage e.g. plastics and car

conting materials that experience up damage e.g. plastics and car

conting materials that experience molecules, photon traps, UV sinks or

conting markers, general reporter molecules, photon traps, UV sinks or

conting species, and in fruits and vegetables to enhance their

characterials the Netschelbes to enhance their

chromophore to be isolated was Green Fluorescent protein (GFP). The

current sequence represents the Neterminal amino acid sequence of a

colour-facilitating molecule (CFM)
 0
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 Colour facilitating molecule, CFM; green fluorescent protein, GFP; chromophore; biomatrix; transgenic animal; colouring agent; flower industry; expression marker; reporter molecule; photon trap;
 ..
0
 100.0%; Score 21; DB 5; Length 16; 100.0%; Pred. No. 42; 0; Indels ive 0; Mismatches 0; Indels
 Dove SG;
 N-terminal amino acid sequence of a CFM #14.
 Brugliera F, Mason J,
Prescott M;
 ABB99074 standard; peptide; 16 AA.
 Claim 4; Page 281; 510pp; English.
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 2001US-0273227P.
 01-MAR-2002; 2002WO-GB000928
 (first entry)
 5; Conservative
 (UYQU) UNIV QUEENSLAND. (JONE/) JONES E L.
 Jones EL, Karan M,
Hoegh-Guldberg IO,
 WPI; 2002-740765/80.
 UV sink; sunscreen.
 Local Similarity
 (NUFA-) NUFARM LID
 1 SVIAK 5
 Ŋ
 Sequence 16 AA;
 SVIAK
 22-JAN-2003
12-SEP-2002
 ABB99074;
 Query Match
 white
 Matches
 ABB99074
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous convention to particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or ced coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other cuses include transducing or intensifying an image, providing additional light for growing photorropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include, expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or cornamental fungal species, and in fruits and vegetables to enhance their contemplated to shoult the specien contemplated susage and the first all-protein contemplate sequence be isolated was Green Fluorescent protein (GFP). The current sequence represents the N-terminal amino acid sequence of a
 Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 Gaps
 .,
 100.0%; Score 21; DB 5; Length 16; 100.0%; Pred. No. 42; 0; Indels ive 0; Mismatches 0; Indels
 /note= "Xaa is any amino acid except Lys"
 /label= Xaa
/note= "Xaa is any amino acid except Met"
 /note= "Xaa is any amino acid except Val"
 Mason J, Dove SG;
 Location/Qualifiers
 Brugliera F,
Prescott M;
 colour-facilitating molecule (CFM)
 Claim 4; Page 282; 510pp; English.
 02-MAR-2001; 2001US-0273227P.
21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 01-MAR-2002; 2002WO-GB000928
 label= Xaa
 /label= Xaa
 Local Similarity 100.
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 Hoegh-Guldberg IO,
 (JONE/) JONES E L.
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 Misc-difference
 Misc-difference
 Misc-difference
 Sequence 16 AA;
 SVIAK
 1 SVIAK
 WO200270703-A2
 white light.
 12-SEP-2002
 Query Match
 Jones
 Matches
g
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RESULT 8

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us-09-890-463-1.rag

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Novel color-facilitating molecule for producing a biomatrix, has a polypeptide which alone/along with molecules imparts altered visual characteristics to cells in the absence of excitation by extraneous non-
 chromophore, biomatrix, transgenic animal, colouring agent,
flower industry, expression marker, reporter molecule, photon trap,
 Colour facilitating molecule; CFM; green fluorescent protein; GFP;
 100.0%; Score 21; DB 5; Length 16; 100.0%; Pred. No. 42; 0; Indels cive 0; Mismatches 0; Indels
 Mason J, Dove SG;
 N-terminal amino acid sequence of a CFM #12.
 Brugliera F,
Prescott M;
 Claim 4; Page 281; 510pp; English.
 ABB99072 standard; peptide; 16 AA
 01-MAR-2002; 2002WO-GB000928.
 02-MAR-2001; 2001US-0273227P.
 21-MAR-2001; 2001AU-00003874.
15-OCT-2001; 2001US-0329816P.
 (first entry)
 (NUFA-) NUFARM LTD.
(UYQU) UNIV QUEENSLAND.
 Karan M,
 WPI; 2002-740765/80
 UV sink; sunscreen
 Hoegh-Guldberg IO,
 (UYQU) UNIV QUEEN (JONE) JONES E L.
 Sequence 16 AA;
 WO200270703-A2.
 Unidentified
 22-JAN-2003
 12-SEP-2002
 white light
 Jones EL,
 ABB99072;
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The invention relates to an isolated colour-facilitating molecule (CFM) comprising a polypeptide which, in a cell, alone or together with one or more other molecules imparts an altered visual characteristic to the cell when visualised by a human eye in the absence of excitation by extraneous non-white light or particle emission. CFMs are useful for producing a transgenic animal which exhibits a novel colour e.g. sheep with blue or red coloured fleece. They are useful for producing coloured plant extracts, e.g. flavouring, beverage or juice or colouring agent. Other uses include transducing or intensifying an image, providing additional light for growing phototropic organisms e.g. algae and/or corals, for coating materials that experience UV damage e.g. plastics and car upholstery. CFMs are useful in the flower industry, in the development of new varieties of flowering plants. Other contemplated uses include,
 expression markers, general reporter molecules, photon traps, UV sinks or in sunscreens. CFMs modify visible colour in edible and/or ornamental fungal species, and in fruits and vegetables to enhance their marketability. CFMs embedded in a gel matrix improve image quality in situations of distorted light spectra (biomatrix). The first all-protein current sequence represents the N-terminal amino acid sequence of a colour-facilitating molecule (CFM).
```

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0
 N-terminal, pigment protein from coral tissue, PPCT, fluorescence, tissue marker, fluorescent marker, dyestuff, sunscreen, ultra violet, UV filter.
 Gaps
 0;
 100.0%; Score 21; DB 3; Length 17; 100.0%; Pred. No. 45; ative 0; Mismatches 0; Indels
 Pigment protein from coral tissue N-terminal peptide 3.
 AAY97151 standard; peptide; 18 AA.
 04-DEC-2000 (first entry)
Ouery Match
Best Local Similarity 100...
5; Conservative
 1 SVIAK 5
 1 SVIAK
 AAY97151;
 RESULT 10
 AAY97151
 à
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Acropora aspera.

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Gaps

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Conservative

1 SVIAK 5 SVIAK 5

The N-terminal peptides shown in AAY97147-48 are from pigment protein irradiation Lissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to fallow gene expression in transformed tissues) or general dyestuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters (both claimed).

Sequence 17 AA;

Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.

Claim 4; Page 42; 49pp; English.

N-terminal; pigment protein from coral tissue; PPCT; fluorescence; tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet; UV filter.

Acropora horrida.

WO200046233-A1.

10-AUG-2000.

02-FEB-2000; 2000WO-AU000056.

99AU-00008463

02-FEB-1999;

Hoegh-Guldberg O, Dove S;

(UNSY ) UNIV SYDNEY.

WPI; 2000-532892/48.

Pigment protein from coral tissue N-terminal peptide 2.

04-DEC-2000 (first entry)

AAY97148;

AAY97148 standard; peptide; 17 AA.

RESULT 9

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1 SVIAK 5
 Ŋ
 SVIAK
 Sequence 25 AA;
 Bernstein HS,
 Homo sapiens
 US6183961-B1
 18-SEP-1998;
 22-SEP-1997;
 06-FEB-2001.
 AAB62002;
 Query Match
 Matches
 RESULT 12
 AAB62002
à
 g
 0
 The N-terminal peptides shown in AAY97151-52 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and maximal fluorescence emission is in the range of 11m. PPCT may be used as a tissue marker, fluorescent marker (e.g. to follow gene expression in transformed tissues) or general dysetuff (all claimed). PPCT may also be used in munscreen formulations or UV filters
 Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 N-terminal, pigment protein from coral tissue; PPCT; fluorescence; tissue marker; fluorescent marker; dyestuff; sunscreen; ultra violet; UV filter.
 Gaps
 ,
0
 DB 3; Length 18;
 0; Indels
 Pigment protein from coral tissue N-terminal peptide 4.
 48;
 Mismatches
 Score 21;
Pred. No. 4
 AAY97152 standard; peptide; 25 AA.
 Example 2; Page 18; 49pp; English.
 100.0%; Sc
100.0%; Pr
tive 0;
 02-FEB-2000; 2000WO-AU000056.
 99AU-00008463.
 99AU-00008463
 02-FEB-2000; 2000WO-AU000056
 Hoegh-Guldberg O, Dove S;
 Hoegh-Guldberg O, Dove S;
 (first entry)
 5; Conservative
Montipora caliculata.
Porites murrayensis.
 (UNSY) UNIV SYDNEY.
 WPI; 2000-532892/48.
 (UNSY) UNIV SYDNEY.
 WPI; 2000-532892/48.
 Query Match
Best Local Similarity
 1 SVIAK 5
 SVIAK 5
 Sequence 18 AA;
 WO200046233-A1.
 WO200046233-A1.
 Porites lobata
 claimed)
 02-FEB-1999;
 02-FEB-1999;
 04-DEC-2000
 10-AUG-2000
 10-AUG-2000
 AAY97152;
 (both
 Best Loc
Matches
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0
 The N-terminal peptides shown in AAY97151-52 are from pigment protein from coral tissue (PPCT). PPCT is capable of emitting fluorescence upon irradiation by incident light whose maximal absorbance is in the range of 320-600 nm and a maximal fluorescence emission is in the range of 300-700 nm. PPCT may be used as a tissue marker, fluorescent marker (e.g. to close follow gene expression in transformed tissues) or general dyestuff (all claimed). PPCT may also be used in sunscreen formulations or UV filters (both claimed)
 The invention relates to a human Cdc5 (hCdc5) protein. The hCdc5 cDNA is useful in the therapy of pathologies such as diseases, syndromes, or other undesirable conditions resulting from defects in cell cycle progression which may result from hCdc5 gene, in the regulation of the expression of the hCdc5 gene or in a step downstream of hCdc5 in the regulation of cell cycle progression through G2 and entry into mitosis. It is useful for treating a patient having a hyperproliferative disease such as cancer, coronary artery disease, pulmonary vascular obstructive disease, and other disorders of abnormal cellular proliferation (see AAB61997 for various used of the hCdc5 gene). The present sequence represents a fragment of the c-myb protein, used for amino-terminal
Novel pigment protein derived from corals capable of emitting fluorescence upon irradiation by incident light useful as tissue marker, fluorescent marker or general dyestuff.
 Novel nucleic acids comprising human Cdc5 gene useful in gene therapy techniques for treating diseases related to cell cycle defect such as cancer, coronary artery disease, pulmonary obstructive vascular disease.
 Cdc5; hCdc5 cell cycle progression; hyperproliferative; cancer; human; coronary artery disease; cellular proliferation; cardiac injury; C-myb; myocardial infarction; cytostatic; cardiant; vasotropic; gene therapy.
 Gaps
 .
0
 100.0%; Score 21; DB 3; Length 25; 100.0%; Pred. No. 70; cive 0; Mismatches 0; Indels
 C-myb protein fragment (residues 92-141).
 AAB62002 standard; protein; 50 AA.
 Example 2; Page 18; 49pp; English.
 Disclosure; Fig 2B; 45pp; English.
 98US-00156316.
 97US-0060688P
 Coughlin SR;
 14-MAY-2001 (first entry)
 5; Conservative
 (REGC) UNIV CALIFORNIA.
 WPI; 2001-210295/21.
 Best Local Similarity
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Page

us-09-890-463-1.rag

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Sequence 73 AA;
 SO
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 0;
 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed senses. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders polypeptide and polynucleotide sequences have applications in properties.
 diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
 Gaps
 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 .;
0
 Score 21; DB 4; Length 50; Pred. No. 1.5e+02;
 0; Indels
 0; Mismatches
 Claim 20; SEQ ID NO 44421; 103pp; English.
 Novel human diagnostic protein #14053.
homology studies with hCdc5 protein
 ABG14062 standard; protein; 73 AA.
 100.0%;
100.0%;
 Tang YT;
 30-MAR-2001; 2001WO-US008631.
 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
 (first entry)
 5; Conservative
 WPI; 2001-639362/73.
 Drmanac RT, Liu C,
 Query Match
Best Local Similarity
 26 SVIAK 30
 (HYSE-) HYSEQ INC.
 1 SVIAK 5
 N-PSDB; AAS78249
 Sequence 50 AA;
 WO200175067-A2.
 biodiversity.
 Homo sapiens.
 18-FEB-2002
 11-OCT-2001.
 ABG14062;
 Matches
 RESULT 13
 ABG14062
 SXS
 ð
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·.
 designated ORF (Open reading frame) 1-4534, more more approach and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses ABN79587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORFAT-ORF4534 (collectively) referred to as ORFX) proteins, polypuroleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polymocleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, enchods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopoiesis regulation, tissue growth, anglogenesis, activin or inhibin activity, chemotactic/
 Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; mandulation; haematopolesis regulation; tissue growth; angloantion; hamanatopolesis regulation; tissue growth; angloantion; dimbin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; cardiovascular disease; immune system disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; wasotropic; antipsoriatic, antidiabetic; cytostatatic; notropic; neuroprotective; antithatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
 Gaps
 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
 0;
 Sequences ABP31028-ABP35561 represent 4534 novel human proteins
100.0%; Score 21; DB 4; Length 73; 100.0%; Pred. No. 2.4e+02;
 0; Indels
 Human isomerase-like ORF3392 protein, SEQ ID NO:6784.
 100.0%; Prec. ...
 Claim 10; Page 1943; 2508pp; English.
 ABP34419 standard; protein; 73 AA.
 24-MAY-2001; 2001WO-US017076.
 24-MAY-2000; 2000US-0206690P
 09-JUL-2002 (first entry)
 5; Conservative
 Leach MD, Shimkets RA;
 (CURA-) CURAGEN CORP.
 WPI; 2002-106200/14.
N-PSDB; ABN78445.
 Best Local Similarity
 24 SVIAK 28
 1 SVIAK 5
 transplantation
 WO200190366-A2
 Homo sapiens.
 29-NOV-2001.
 ABP34419;
Query Match
 Matches
 RESULT 14
ABP34419
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cc chemokinetic activity, haemostatic activity, thrombolytic activity, creeptor/ligand, antinflammatory activity, tumour inhibition activity, and analy also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, concluded and antibodies may be used in the treatment of cancers, other proliferative disorders such as psoriasis and benign tumours, conter proliferative disorders such as psoriasis and benign tumours, content proliferative disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, content and infectious diseases caused by viral, bacterial, content and other pathogens. ORFX uncleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous contents of the identification and cloning of homologous contents and probes, in the detection of organs activity of ORFX uncleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the content and monitoring of ORFX-associated diseases
 Sequence 73 AA;
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0
 Gaps
 ..
100.0%; Score 21; DB 5; Length 73; 100.0%; Pred. No. 2.4e+02; tive 0; Mismatches 0; Indels
 5; Conservative
 Query Match
Best Local Similarity
 Matches
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64 SVIAK 68 1 SVIAK 5 ð d

ABP77483 standard; protein; 75 AA. ABP77483; RESULT 15 ABP77483 

(first entry) 07-MAR-2003 N. gonorrhoeae amino acid sequence SEQ ID 1496.

Antibacterial; infection; vaccine; gene therapy

Neisseria gonorrhoeae.

WO200279243-A2.

10-OCT-2002

12-FEB-2002; 2002WO-IB002069.

12-FEB-2001; 2001GB-00003424.

(CHIR-) CHIRON SPA.

Masignani V, Monaci E; Fontana MR, Pizza M, WPI; 2003-058415/05.

N-PSDB; ABZ38453.

Disclosure, Page 296, 815pp, English.

New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection.

The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid

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molecules of the invention
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Sequence 75 AA;

Gaps ., Length 75; 0; Indels 100.0%; Score 21; DB 6; I 100.0%; Pred. No. 2.4e+02; rative 0; Mismatches 0; Query Match Best Local Similarity luv... S; Conservative

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1 SVIAK 5

30 SVIAK 34 ð g Search completed: August 12, 2004, 06:17:04 Job time : 3.89549 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
 Copyright
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OM protein - protein search, using sw model

August 12, 2004, 06:19:43; Search time 10.5225 Seconds (without alignments) 149.169 Million cell updates/sec Run on:

US-09-890-463-1 21 1 SVIAK 5

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1292805 seqs, 313927144 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:\*

| cgn2\_6/ptodata/2/pubpaa/USO7\_PUBCOMB.pep:\*
2: /cgn2\_6/ptodata/2/pubpaa/USO6\_NEW PUB.pep:\*
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4: /cgn2\_6/ptodata/2/pubpaa/USO6\_PUBCOMB.pep:\*
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12: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
13: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
14: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
15: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
16: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
17: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
18: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*
18: /cgn2\_6/ptodata/2/pubpaa/USO8\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|     | Description              | Segmence 6. Appli | Sequence 14. Aprol | Sequence 235707.     | Sequence 201620.     | Sequence 281604.     | Segmence 259733.     | Segmence 6784. An   | Segmence 2542. An  | Segmence 196. Ann | Sequence 196. App | Sequence 196. App  | Sequence 200366.     | Semience 252896      | Semience 39108      | Sequence 4, Appli |
|-----|--------------------------|-------------------|--------------------|----------------------|----------------------|----------------------|----------------------|---------------------|--------------------|-------------------|-------------------|--------------------|----------------------|----------------------|---------------------|-------------------|
|     | ID                       | US-09-757-049A-6  | US-09-912-962-14   | US-10-424-599-235707 | US-10-437-963-201620 | US-10-424-599-281604 | US-10-424-599-259733 | US-09-864-408A-6784 | US-10-276-774-2542 | US-09-738-973-196 | US-09-854-133-196 | US-10-144-649A-196 | US-10-424-599-200366 | US-10-424-599-252896 | US-10-425-114-39108 | US-09-892-398-4   |
|     | DB                       | 6                 | σ                  | 12                   | 16                   | 12                   | 12                   | 11                  | 12                 | σ                 | σ                 | 14                 | 12                   | 12                   | 12                  | 10                |
|     | Query<br>Match Length DB | 50                | 52                 | 55                   | 63                   | 99                   | 72                   | 73                  | 76                 | 102               | 102               | 102                | 107                  | 138                  | 142                 | 156               |
| οķο | Query<br>Match           | 100.0             | 100.0              | 100.0                | 100.0                | 100.0                | 100.0                | 100.0               | 100.0              | 100.0             | 100.0             | 100.0              | 100.0                | 100.0                | 100.0               | 100.0             |
|     | Score                    | 21                | 21                 | 21                   | 21                   | 21                   | 21                   | 21                  | 21                 | 21                | 21                | 21                 | 21                   | 21                   | 21                  | 21                |
|     | Result<br>No.            | Н                 | 7                  | e                    | 4                    | Ŋ                    | ٥                    | 7                   | 80                 | 6                 | 10                | 11                 | 12                   | 13                   | 14                  | 15                |

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RESULT 2
US-09-912-962-14
Sequence 14, Application US/09912962
Patent No. US20020076719A1
GENERAL INFORMATION:

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| Sequence 46, Appl<br>Sequence 283302,<br>Sequence 280513,<br>Sequence 10328, A          |                                                                  | Sequence 72020, A<br>Sequence 72021, A<br>Sequence 209489,<br>Sequence 9990, Ap<br>Sequence 252176. |                                                                         | Sequence 63475, A<br>Sequence 374, App<br>Sequence 33397, A<br>Sequence 71886, A<br>Sequence 71886, A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Sequence 14819, A Sequence 121, App Sequence 121, App Sequence 6, Appli Sequence 6, Appli Sequence 942, App Sequence 816, App                    |
|-----------------------------------------------------------------------------------------|------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------|
| US-09-892-398-46<br>US-10-424-599-283302<br>US-10-424-599-280513<br>US-10-369-493-10328 | 10-437-963-13<br>10-424-599-23<br>10-425-114-64<br>10-424-599-18 | -10-42<br>-10-42<br>-10-42<br>-10-15                                                                | -10-369-493-21085<br>-10-156-275-88<br>-09-935-338-105<br>-10-380-430-9 | 5-10-282-1224-634<br>5-10-287-226-374<br>5-10-425-114-5339<br>5-10-425-114-7188                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | US-09-864-761-3419<br>US-09-886-055-121<br>US-09-804-291-121<br>US-09-844-861A-6<br>US-10-343-650A-206<br>US-10-017-161-942<br>US-10-292-798-816 |
| 122                                                                                     | 92225                                                            | 4444                                                                                                | 11011                                                                   | 12 12 12 12 12 12 12 12 12 12 12 12 12 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 2 6 1 1 1 1 1 2 4 1 1 1 2 4 1 1 1 1 1 1 1 1                                                                                                      |
| 156<br>161<br>165<br>165                                                                | 169<br>1989<br>193                                               | 196<br>196<br>208<br>233<br>242                                                                     | 244<br>249<br>260<br>260<br>263                                         | 283338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>2836<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>2838<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>2836<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>28338<br>2836<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>2836<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>28358<br>2836 |                                                                                                                                                  |
| 100.0<br>100.0<br>100.0                                                                 | 100.0<br>100.0<br>100.0                                          | 100.0                                                                                               | 100.0<br>100.0<br>100.0                                                 | 100.00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 100.0<br>100.0<br>100.0<br>100.0                                                                                                                 |
| 21<br>21<br>21<br>21                                                                    | 22222                                                            | 22222                                                                                               | 22222                                                                   | 122222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 222222222222222222222222222222222222222                                                                                                          |
| 16<br>17<br>18<br>19                                                                    | 20<br>23<br>23<br>23<br>23                                       | 2 2 2 5 1<br>2 2 4 6 5 1                                                                            | 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3                                   | # # # # # # # # # # # # # # # # # # #                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 2 4 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5                                                                                                          |

## ALIGNMENTS

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Sequence 6, Application US/09757049A
| Sequence 6, Application US/09757049A
| Patent No. US20020127702A1
| GENERAL INFORMATION:
| APPLICANT: BERNSTEIN, Harold S. |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING CELL CYCLE |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING CELL CYCLE |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING CELL CYCLE |
| TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR REGULATING DATE: US/09/156,316 |
| PRIOR PELICATION NUMBER: US/09/156,316 |
| PRIOR PELICATION NUMBER: US/09/156,316 |
| PRIOR PELIUNG DATE: 1998-09-18 |
| PRIOR PELIUNG DATE: 1998-09-18 |
| PRIOR PELIUNG DATE: 1997-09-22 |
| NUMBER OF SEQ ID NOS: 50 |
| SEQ ID NO 6 |
| LENGTH: 50 |
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Best Local Similarity 100.
Matches 5; Conservative
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-757-049A-6
RESULT 1
US-09-757-049A-6
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TITLE OF INVENTION: 1.1, Ping;
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement;
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILICATION NUMBER: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 201620
LENGTH: 63
TYPP:
TYPP:
 Sequence 281664, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 1003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 281604
LENGTH: 66
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 Length 66;
 Length 63;
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 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_96978C.1.pep
US-10-437-963-201620
 ; CTHER INFORMATION: Clone ID: PAT_MRT3847_96309C.1.pep
US-10-424-599-281604
 Query Match
100.0%; Score 21; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0;
 100.0%; Score 21; DB 12;
100.0%; Pred. No. 2.2e+02;
cive 0; Mismatches 0;
 100.0%; Score 21; DB 16;
100.0%; Pred. No. 2.6e+02;
vative 0; Mismatches 0;
 US-10-437-963-201620
Sequence 201620, Application US/10437963
Publication No. US20040123343A1
SERBEAL INFORMATION:
APPLICANT: LA Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
 5; Conservative
 Conservative
 ORGANISM: Oryza sativa
 TYPE: PRT
ORGANISM: Glycine max
 Query Match
Best Local Similarity
.-heq 5; Conserv?
 Query Match
Best Local Similarity
 22 SVIAK 26
 25 SVIAK 29
 1 SVIAK 5
 1 SVIAK 5
 RESULT 5
US-10-424-599-281604
US-10-424-599-235707
 RESULT 4
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 Sequence 235707, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Con Vinua
APPLICA
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0
 Smogorzewska, Agata
Smogorzewska, Agata
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
 COMPUTER KEADMALE FORMY

MEDIUM TYPE: FIOPPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/912,962

FILING DATE: 25-Jul-2001

CLASSIFICATION CONTROWN>

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 09/018,635

FILING DATE: 04-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: DAVIA A. Jackson

RESPERENCE/DOCKET NUMBER: 600-1-142 CIP1

TELEPHONE: 201-487-5800

TELEPHONE: 201-33-1684

TELEEX: 133521
 Query Match
100.0%; Score 21; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
 OTHER INFORMATION: Clone ID: PAT_MRT3847_54872C.1.pep
 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: KAAUBER & JACKSON
STREET: 411 Hackensack Avenue
CITY: Hackensack
 LENGTH: 52 amino acids
 APPLICANT: de Lange, Titia
Broccoli, Domin
 TYPE: amino acid
STRANDEDNESS: single
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 52
 STATE: New Jersey
COUNTRY: USA
 ORGANISM: Glycine max
 27 SVIAK 31
 1 SVIAK 5
 RESULT 3
US-10-424-599-235707
 SEQ ID NO 235707
LENGTH: 55
 US-09-912-962-14
 FEATURE:
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 0
 APPLICANT: Hyeeq, Inc.
APPLICANT: Tang, Y, Tom et al
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUSCOM
 Gaps
 0
 0
 APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILLE REPERBURE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
 Length 76;
 100.0%; Score 21; DB 9; Length 102; 100.0%; Pred. No. 4.38+02; ive 0; Mismatches 0; Indels
 Indels
 CTHER INFORMATION: Xaa = any amino acid or nothing US-10-276-774-2542
 Query Match 100.0%; Score 21, DB 12; Best Local Similarity 100.0%; Pred. No. 3.2e+02; Matches 5; Conservative 0; Mismatches 0;
 NUMBER OF SEQ ID NOS: 587
SOFTWARE: PastSEQ for Windows Version 3.0
Sequence 2542, Application US/10276774 Publication No. US20040053245A1 GENERAL INFORMATION:
 Sequence 196, Application US/09738973
Patent No. US20020110563A1
PAPPLICANT: Reed, Steven G.
 Algate, Paul A.
Secrist, Heather
Indirias, Carol Yoseph
Benson, Darin R.
Elliot, Mark
 Reed, Steven G.
Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
 5; Conservative
 NAME/KEY: misc feature
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Homo sapien
 Query Match
Best Local Similarity
Matches 5; Conserv
 24 SVIAK 28
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 1 SVIAK 5
 US-09-738-973-196
 US-09-738-973-196
 SEQ ID NO 2542
LENGTH: 76
 SEQ ID NO 196
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
 TYPE: PRT
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 US-10-424-599-259733

US-10-424-599-259733

Sequence 259733, Application US/10424599

SUBLICATION: US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Car Orongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(5223)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 259733
 Sequence 6784, Application US/09864408A.

Publication No. US20040009474A1

GENERAL INFORMATION:

Publication No. US20040009474A1

GENERAL INFORMATION:

APPLICANT: Leach, Martin D.

APPLICANT: Care of the control of t
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 LOCATION: (17) ... (17) ... (17) ... (17) ... OTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid US-09-864-408A-6784
 Gaps
 0; Gaps
 .
 100.0%; Score 21; DB 11; Length 73; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
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US-10-424-599-259733
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Matches 5; Conservative
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ORGANISM: Homo sapiens
 NAME/KEY: misc_feature
 TYPE: PRT
ORGANISM: Glycine max
 Best Local Similarity
Matches 5; Conserv
 32 SVIAK 36
 64 SVIAK 68
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 1 SVIAK 5
 1 SVIAK 5
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US-09-864-408A-6784
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-21(5223)B; CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 200366
LENGTH. 100
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 Length 107;
 Length 138;
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 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_22957C.1.pep
US-10-424-599-200366
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_70391C.1.pep
US-10-424-599-252896
 100.0%; Score 21; DB 12;
100.0%; Pred. No. 6e+02;
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 100.0%; Score 21; DB 12;
100.0%; Pred. No. 4.6e+02;
iive 0; Mismatches 0;
 LOCATION: (1)..(107)
OTHER INFORMATION: unsure at all Xaa locations
 US-10-425-114-39108

Sequence 39108, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Kovalic, David K.

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E.
 Ouery Match
Best Local Similarity 100.vv
Thes 5; Conservative
 Conservative
 TYPE: PRT ORGANISM: Glycine max
 ORGANISM: Glycine max
 Query Match
Best Local Similarity
5, Conserv?
 125 SVIAK 129
 1 SVIAK 5
 1 SVIAK 5
 SVIAK 9
 FEATURE:
NAME/KEY: unsure
 US-10-424-599-252896
 SEQ ID NO 252896
 LENGTH: 138
 FEATURE:
 RESULT 14
 RESULT 13
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 Sequence 196, Application US/10144649A
| Publication No. US20030118599A1
| General Information in US2003011859A1
| General Information in US2003011859A1
| General Information in US2003011859A1
| APPLICANT: Mang, Tongtong | APPLICANT: Fan, Liqun | APPLICANT: Fan, Liqun | APPLICANT: McNeill, Patricia D. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.475c11 | CURRENT FILING DATE: 2002-08-21 | UNMBER OF SEQ ID NOS: 749 | SOFTWARE FEASER for Windows Version 3.0 | SEQ ID NO 196 | LUNG CANCER | LUNG CANCER | LUNG CANCER | LUNG CANCER | SEQ ID NOS: 749 | SOFTWARE FEASER for Windows Version 3.0 | LUNG CANCER | SEQ ID NOS: 749 | SOFTWARE PASSER for Windows Version 3.0 | LUNG CANCER | LU
 0;
 0;
 100.0%; Score 21; DB 14; Length 102; 100.0%; Pred. No. 4.3e+02; cive 0; Mismatches 0; Indels
 APPLICANT: Lodges, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Darin R.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
 Length 102;
 100.0%; Score 21; DB 9; Length 10
100.0%; Pred. No. 4.3e+02;
iive 0; Mismatches 0; Indels
 CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SEQ ID NO 196
LENGTH: 102
 Sequence 200366, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Evoalic David K
APPLICANT: Zhou Yihua
 Sequence 196, Application US/09854133
Publication No. US20020183499A1
GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conservative
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 TYPE: PRT
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 44 SVIAK 48
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 1 SVIAK 5
 US-10-424-599-200366
 US-10-144-649A-196
 US-10-144-649A-196
 US-09-854-133-196
 US-09-854-133-196
 Query Match
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Sequence 252896, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREBENCE: 38-21(53233)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
 APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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Gaps
 Gaps
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0
 Gaps
 0;
 Query Match
100.0%; Score 21; DB 12; Length 142;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels (
 NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STATE: New Jersey
COUNTRY: USA
ZIP: 07601
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/892,398
FILING DATE: 27-Jun-2001
CLASSIFICATION: AUDATA:
APPLICATION NUMBER: 09/280,590
FILING DATE: CURROWN:
APPLICATION NUMBER: 09/280,590
FILING DATE: CURROWN:
APPLICATION NUMBER: 20-442
REGISTRATION NUMBER: 20-442
REGISTRATION NUMBER: 20-442
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 Bodner, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
THEREOF
 ; FEATURE:
; OTHER INFORMATION: Clone ID: 700208712_FLI.pep
US-10-425-114-39108
 ORGANISM: Mus musculus
;
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-892-398-4
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
LENGTH: 142
 RESULT 15
US-09-892-398-4
; Sequence 4, Application US/09892398
; Publication No. US20030028002A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Hiroshi
; Sherr, Charles
; Sherr, Charles
; Sherr, Charles
; Sherr, Charles
 TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLIOGY: linear
MOLECULE TYPE: protein
HYPOCHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
 LENGTH: 156 amino acids
 CITY: Hackensack
 TYPE: PRT
ORGANISM: Zea mays
 |||||
41 SVIAK 45
 1 SVIAK 5
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Ouery Match
Best Local Similarity 100.0%; Score 21; DB 10; Length 156;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 SVIAK 5
Db 79 SVIAK 83
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Search completed: August 12, 2004, 06:51:20 Job time : 10.5225 secs

(oldsu) Andla egod sidi

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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| protein             |
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August 12, 2004, 06:12:47; Search time 1.30123 Seconds (without alignments) 1212.385 Million cell updates/sec Run on:

US-09-890-463-1 21 1 SVIAK 5

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp\_plant: \*
sp\_rodent: \*
sp\_virus: \*
sp\_vrtcbrate: \*
sp\_unclassified: \*
sp\_virus: \*
sp\_rvirus: \*
sp\_archerap: \* 10: 11: 12: 13:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |     |        | Description     | Ogxt66 canis famil | OBOTTA STANDY | OBerras states | OBOACE MADE TO DESCRIBE | Oznibe aphelenching | Ogogan missing | Oobido hide musculu | Cond 2 Daccer Toplia | Cacala musculu | 017211 caenorhabdi | O8sc48 stx2 conver | O8e7b3 strentococo | OBODA DESCRIPTION | Contract of the Contract of th | Usvk36 mycobacter1 | O7u080 mycobarteri | Obvide hactorionha | O8zv15 pvrobaculum |
|-----------|-----|--------|-----------------|--------------------|---------------|----------------|-------------------------|---------------------|----------------|---------------------|----------------------|----------------|--------------------|--------------------|--------------------|-------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES |     |        | ID              | O9XT66             | OSCRIG        | OBEVWS         | O8P4C6                  | O7YUBB              | 092227         | OBHA:T2             | C + 0 C a C          | Cacada         | 01/211             | Q8SC48             | O8E7B3             | 089948            | 7674140                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | CO NTO             | Q7U080             | 90fX60             | Q8ZVL5             |
|           |     |        | DB              | 9                  | 16            | 16             | 16                      | Ŋ                   | 11             | 6                   | , [                  | 4 1            | n                  | 6                  | 16                 | 16                | 9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 7                  | 76                 | 6                  | 17                 |
|           |     |        | Match Length DB | 63                 | 75            | 95             | 98                      | 107                 | 111            | 126                 | 126                  | 1 1            | 132                | 135                | 141                | 141               | 152                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 1                  | 152                | 161                | 161                |
|           | οķο | Query  | Match           | 100.0              | 100.0         | 100.0          | 100.0                   | 100.0               | 100.0          | 100.0               | 1000                 |                | 0.00               | 100.0              | 100.0              | 100.0             | 100                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                    | 100.0              | 100.0              | 100.0              |
|           |     |        | Score           | 21                 | 21            | 21             | 21                      | 21                  | 21             | 21                  | 21                   | 16             | T 7                | 21                 | 21                 | 21                | 21                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                    | 77                 | 21                 | 21                 |
|           |     | Result | No.             | 1                  | 7             | m              | 4                       | ហ                   | 9              | 7                   | œ                    | σ              | ,                  | 10                 | 11                 | 12                | 13                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                    | 14                 | 15                 | 16                 |

| Q8ha15 bacteriopha | O8exa9 lentospira |        | OShae Salmonalla |        | 09n436 aiellomynes | 090433 aiellomyces | 090439 aiellomyces | O90435 aiellomydes | O9D437 arellomyces |        | 167    | 7      |        | 099v25 stanhvlocod |        |        |        |        |        | Ω      | m      |        | O8fsil corvnebacte |        | 09f8v9 agrobacteri | 095p04 goniopora t | 09ahz2 photorhabdu | Q69112 herpes simp |
|--------------------|-------------------|--------|------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|
| Q8HA15             | Q8EXA9            | Q98R43 | OSHAES           | 000300 | O9P436             | 092433             | 092439             | Q9P435             | Q9P437             | Q9P434 | P87467 | Q9CVJ7 | 087751 | Q99V25             | OBNX89 | P97753 | Q8R852 | 086813 | Q9AAV8 | 052946 | Q8Y9M4 | Q9SW28 | Q8FSI1             | Q9N6J5 | Q9F8V9             | Q95P04             | Q9AHZ2             | 069112             |
| σ                  | 16                | 16     | 0                | m      | m                  | m                  | m                  | m                  | m                  | 3      | 13     | 11     | 16     | 16                 | 16     | 11     | 16     | 16     | 16     | N      | 16     | 10     | 16                 | Ŋ      | 16                 | Ŋ                  | 7                  | 12                 |
| 162                | 164               | 171    | 172              | 175    | 175                | 175                | 175                | 175                | 175                | 175    | 176    | 177    | 181    | 188                | 188    | 191    | 192    | 196    | 197    | 199    | 200    | 203    | 209                | 218    | 219                | 221                | 223                | 224                |
| 100.0              | 100.0             | 100.0  | 100.0            | 100.0  | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0  | 100.0  | 100.0  | 100.0  | 100.0              | 100.0  | 100.0  | 100.0  | 100.0  | 100.0  | 100.0  | 100.0  | 100.0  | 100.0              |        | 100.0              | 100.0              | 100.0              | 100.0              |
| 21                 | 21                | 21     | 21               | 21     | 21                 | 21                 | 21                 | 21                 | 21                 | 21     | 21     | 21     | 21     | 21                 | 21     | 21     | 21     | 21     | 21     | 21     | 21     | 21     | 21                 | 21     | 21                 | 21                 | 21                 | 21                 |
| 17                 | 18                | 19     | 20               | 21     | 22                 | 23                 | 24                 | 25                 | 26                 | 27     | 28     | 29     | 30     | 31                 | 32     | 33     | 34     | 35     | 36     | 37     | 38     | 39     | 40                 | 41     | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

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PROSITE; PS00831; RIBOSOMAL_L27; 1.
TIGRFAMS; TIGR00062; L27; 1.
 NCBI_TaxID=340;
 Hypothetical
 SEQUENCE
 Query Match
 Query Match
Best Local S
 Q8P4C6
Q8P4C6;
 Matches
 Matches
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 RESULT 4
Q8P4C6
 RESULT 9
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 Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;

"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";

Nucleic Acids Res. 30:5293-5300(2002).

EMBL; AP004171; BAC44234.1; -...
GO; GO:0005840; C:nitracellular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0006412; P:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein blosynthesis; IEA.
 Gaps
 Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z., Chen Z., Wen Y.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AE016749; AA005341.1; --
 Gaps
 Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBL_TaxID=28227;
 ;
 ..
 100.0%; Score 21; DB 16; Length 75; 100.0%; Pred. No. 2.3e+02; rive 0; Mismatches 0; Indels
 Length 63;
 100.0%; Score 21; DB 6; Length 63 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
 te proteome.
9B017C60D9C61D9F CRC64;
 OBEWWS;
01-MAR-2003 (TrEMBirel. 23, Created)
01-MAR-2003 (TrEMBirel. 23, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
Ribosomal protein L27.
 7707 MW; D8C86265802F3C9F CRC64;
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
CONSERVED hypothetical protein.
 Staphylococcus epidermidis.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
 75 AA
 Interpro; IPR001684; Ribosomal_L27.
Pfam; PF01016; Ribosomal L27; I.
PRINTS; PR00063; RIBOSOMĀLL27; I.
ProDom; PD0031144; Ribosomal_L27; 1.
 STRAIN=HF-2;
MEDLINE=22354719; PubMed=12466555;
 Hypothetical protein; Complete
SEQUENCE 75 AA; 8090 MW; 9B
 PRELIMINARY;
 Local Similarity 100.
 PRELIMINARY;
 63
63 AA;
 SEQUENCE FROM N.A. STRAIN=ATCC 12228;
 SEQUENCE FROM N.A.
 71 SVIAK 75
 19 SVIAK 23
 1 SVIAK 5
 1 SVIAK 5
 SEQUENCE
 Query Match
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 QBEVWS
 Matches
 RESULT 2
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 Q8EVW5
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REPORTING PROM N.A.

REPORTING ATCC 33913 (NCPPB 528;

REQUIRE 2202145; PubMed=12024217;

RA MEDINE=2202145; PubMed=12024217;

RA SILVA A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.P.,

RA Alves L.M.C., Monteiro-Vitorello C.B., Van Sluys M.A., El-Dorry H.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Ratsuyama A.M., Mondanis J., Menck C.F. M., Myaki C.Y., Moon D.H.,

Martins E.C., Meidanis J., Menck C.F. M., Myaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Setubal J.C., Kitalina J.P.;

REDI, AE012499; AAM43030.1; -

DR GO; GO:0016020; C:membrane; IRA.

GO; GO:001620; C:membrane; IRA.

GO; GO:0016215; F:transporter activity; IEA.

GO; GO:001698; P:cell wall catabolism; IEA.

DR GO; GO:001698; P:cell wall catabolism; IEA.

DR GO; GO:001698; P:cell wall catabolism; IEA.

DR GO; GO:001627; Lynama Mall Catabolism; IEA.
 Gaps
 Gaps
 Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
 ..
 0;
 100.0%; Score 21; DB 16; Length 98; 100.0%; Pred. No. 38+02; tive 0; Mismatches 0; Indels
 ; Score 21; DB 16; Length 95;
; Pred. No. 2.9e+02;
0; Mismatches 0; Indels
 l protein; Complete proteome.
98 AA; 10593 MW; 0DB6218EB6AAFA60 CRC64;
 95 AA; 10464 MW; 735D951C94B7A730 CRC64;
 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein XCC3784.
 98 AA.
 Pfam; PF01476; LysM; 1. PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
 InterPro; IPR002482; LysM.
InterPro; IPR000531; TonB_boxC.
 100.0%;
 5; Conservative
 Similarity 100.
5; Conservative
 Local Similarity
Complete proteome. SEQUENCE 95 AA;
 56 SVIAK 60
 91 SVIAK 95
 1 SVIAK 5
 1 SVIAK 5
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Gaps

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us-09-890-463-1.rspt

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SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Cerebellum;
MEDLINE=223546813; PubMed=12466851;
The FANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Mature 420:563-573(2002).
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
 Muniesa M., Jofre J.;
"Variability of shiga converting bacteriophages in E. coli O157:H7
"Variability of shiga converting bacteriophages in E. coli O157:H7
strains of human origin isolated from the same outbreak.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS48456; AANS919.1; -.
SEQUENCE 126 AA; 14230 MW; BBF1776A0329F55A CRC64;
 Eukaryota... Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical S-adenosyl-L-methionine-dependent methyltransferases
 100.0%; Score 21; DB 11; Length 126; 100.0%; Pred. No. 3.8e+02; ative 0; Mismatches 0; Indels (
 Length 126;
 Indels
 Hypothetical protein.
SEQUENCE 126 AA; 14568 MW; 0AB92E67189578CD CRC64;
 Last sequence update)
Last annotation update)
 100.0%; Score 21; DB 9; I 100.0%; Pred. No. 3.8e+02;
 132 AA.
 0; Mismatches
 Created)
 PRT;
 PRT;
 EMBL; AK046928; BAC32921.1; -.
MGD; MGI:2442530; 4732479N06Rik.
 structure containing protein.
 01.3AN-1998 (TEMBLEEL 05, 01-JAN-1998 (TEMBLEEL 05, 01-JAN-1998 (TEMBLEEL 05, 01-JUN-2003 (TEMBLEEL 24, C01B12.7 protein.
 Query Match
Best Local Similarity 100.
Matches 5; Conservative
 5; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Caenorhabditis elegans.
 Mus musculus (Mouse)
 Query Match
Best Local Similarity
 NCBI_TaxID=210928;
 SEQUENCE FROM N.A.
 SVIAK 49
 [1]
SEQUENCE FROM N.A.
 1 SVIAK 5
 3 SVIAK 7
 1 SVIAK 5
 NCBI_TaxID=6239;
 STRAIN=159;
 45
 Viruses.
 Q8C8J3;
 Q8C8J3
 017211;
 017211
 Matches
 RESULT 8
 RESULT 9
 Q8C8J3
 017211
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0
 Aphelenchus avenae (Mycophagous nematode).
Eukaryota; Metazoa; Nematoda, Chromadorea; Tylenchida; Aphelenchoidea;
Aphelenchidae; Aphelenchus.
NCBI_TaxID=70226;
 Gaps
 Gaps
 SEQUENCE FROM N.A.

Browne J.A., Goyal K., Tunnacliffe A., Burnell A.;

"Expression of a glutaredoxin gene induced by desiccation and
oxidative stress in the anhydrobiotic nematode Aphelehus avenae.";

Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY340999; AAQ20895.1;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 .
0
 ö
 100.0%; Score 21; DB 11; Length 111; 100.0%; Pred. No. 3.4e+02; Live 0; Mismatches 0; Indels (
 Length 107;
 0; Indels
 Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 20895.1; -.
11614 MW; CB0396A67FEC9C32 CRC64;
 SMART; SM00278; HhH1; 1."
SEQUENCE 111 AA; 12247 MW; E81BBACDF1A3B44F CRC64;
 Last sequence update)
Last annotation update)
 (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 25, Last annotation update)
 Created)
Last sequence update)
Last annotation update)
 100.0%; Score 21; DB 5; I 100.0%; Pred. No. 3.3e+02;
 107 AA.
 111 AA.
 126 AA
 0; Mismatches
 GO; GO:0006916; P:anti-apoptosis; IMP.
GO; GO:0008220; P:necrosis; IMP.
 Created)
 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last seq 01-OCT-2003 (TrEMBLrel. 25, Last ann Similar to DNA polymerase beta.
 PRT;
 PRT;
 PRT;
 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25,
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
 EMBL; BC006681; AAH06681.1;
MGD; MGI:97740; Polb.
 InterPro; IPR003583; HHH 1
 Antitermination protein Q.
 5; Conservative
 Best Local Similarity 100.
Matches 5; Conservative
 PRELIMINARY;
 PRELIMINARY:
 PRELIMINARY;
 Mus musculus (Mouse)
 Q.
Bacteriophage LC159.
 107 AA;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 10 SVIAK 14
 NCBI_TaxID=10090;
 SVIAK 48
 1 SVIAK 5
 1 SVIAK 5
 Glutaredoxin.
GLX-1.
 SEQUENCE
 Query Match
 Q7YUB8;
 Q8HAJ2;
Q7YUB8
 Q922Z7
 Q8HAJ2
 Matches
 RESULT 7
Q8HAJ2
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 21
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 Q89P48
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Matches
 RESULT 12
Matches
 RESULT 11
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STRAIN=Bristol N2;

Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Smaldon N., Smith A., Sonnhammer E., Staden R., Staden R., Shithan J., Weinstook L., Wilkinson-Sproat J., Wohldman P.,

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,

Z. M. De contiguous nucleotide sequence from chromosome III of C.
 Gaps
 STRAIN=Stx2 phage-1;
Sato T., Shimizu T., Matarai M., Kobayashi M., Kano S., Hamabata T.,
Yamaaaki S., Takeda Y.;
"Genomic sequence of Shiga toxin 2-converting phage isolated from
Bscheritchia coll 0.157:H7 Okayama strain and comparison with other
Shiga toxin 2-converting phages."
Shiga toxin 2-converting phages."
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 Hypothetical protein.
Stx2 converting bacteriophage I.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 ;
0
 Length 135;
 Length 132;
 0; Indels
 STRAIN=Bristol N2;
Scheet P., Maggi L.;
"The sequence of C. elegans cosmid CO1B12.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 Waterston R.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
 16106 MW; 15A614C2A739178C CRC64;
 A2C8BA7465940DF2 CRC64;
 Last sequence update)
Last annotation update)
 Score 21; DB 9; 1
Pred. No. 4.1e+02;
 Score 21; DB 5;
Pred. No. 4e+02;
 EMBL, AP004402; BAB87967.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:teansporter activity; IEA.
GO; GO:0006215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
 135 AA
 0; Mismatches
 InterPro; IPR000531; TonB boxC.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
 01-0TW-2002 (TrEMBLrel. 21, Created)
01-0TW-2002 (TrEMBLrel. 21, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
 PRT;
 132 AA; 15750 MW;
 100.0%;
 100.0%;
 EMBL; AF025458; AAB70973.1;
PIR; T32373; T32373.
WormPep; C01B12.7; CE07795.
SEQUENCE 132 AA; 15750 MW
 Query Match
Best Local Similarity 1000.
 PRELIMINARY;
 Nature 368:32-38(1994)
 Hypothetical protein.
SECUENCE 135 AA; 1
 Lambda-like viruses.
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A. STRAIN=Bristol N2;
 NCBI_TaxID=180816;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SVIAK 29
 SVIAK 5
 Q8SC48;
01-JUN-2002
01-JUN-2002
 Н
 25
 SEQUENCE
 Q8SC48
 RESULT 10
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 Gaps
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 STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsurucka H., Wada T., Yamada M.,
 STRAIN=NEM316 / Serotype III;
BEDLINES-2242508; PubMed=-1354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
 "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP065948; BAC48900.1; -.
 "Genome sequence of Streptococcus agalactiae, a pathogen causing
 .;
0
 .
0
 Length 141;
 Length 141;
 Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
 Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Indels
 Indels
 9F10019F39AD214B CRC64;
 Hypothetical protein; Complete proteome.
SEQUENCE 141 AA; 15937 MW; 924D2E86930763F5 CRC64;
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 Last sequence update)
Last annotation update)
 100.0%; Score 21; DB 16;
100.0%; Pred. No. 4.3e+02;
tive 0; Mismatches 0;
 ٥.
 DB 16;
 141 AA
 141 AA.
 Mismatches
 Score 21;
 Created)
 Mol. Microbiol. 45;1499-1513(2002).
EMBL, AL766844; CAD45887.1; -.
 PRT;
 PRT;
 ·
0
 14457 MW;
 100.0%;
 01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
 invasive neonatal disease.
 Conservative
 PRELIMINARY;
 PRELIMINARY;
 Sagalist; gbs0242; -.
 Hypothetical protein.
GBS0242.
 141 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 NCBI TaxID=216495;
 Complete proteome
 SEQUENCE FROM N.A.
 100 SVIAK 104
 SVIAK 25
 1 SVIAK 5
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 01-JUN-2003 (TrE
B113635 protein.
 NCBI_TaxID=375;
 1 SVIAK
 Query Match
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EMBL; BX248338; CAD94218.1; -.
 Complete proteome.
SEQUENCE 152 AA;
 Query Match
Best Local Similarity
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 81 SVIAK 85
 1 SVIAK 5
 37 SVIAK 41
 1 SVIAK 5
 protein.
 90cx60
 Matches
 RESULT 15
 Matches
 901X60
 SOR
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 GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
InterPro; IPR004360; Gly_bleo_diox.
Pfam; PF00903; Glyoxalase; 1.
 Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;
 Gaps
 Gaps
 STRAIN-AF2122/97;
MEDLINE-22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Garnier T., Eiglmeier K., Camus J.-C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
 "Whole genome comparison of Mycobacterium tuberculosis clinical and
 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
4-hydroxyphenylpyruvate dioxygenase C terminal domain containing
 ó:
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0
 Mycobacterium tuberculosis,
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 100.0%; Score 21; DB 16; Length 152; 100.0%; Pred. No. 4.6e+02; ive 0; Mismatches 0; Indels
 Mycobacterium bovis.
Bacteria, Actinobacteridae, Actinomycetales, Corynebacterineae; Mycobacteriaceae, Mycobacterium.
 Indels
 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AERO7009, AAK45627.1; -...
TIGR; MT1364; -...
 Dioxygenase; Pyruvate.
SEQUENCE 152 AA; 16626 MW; 60E64662DC2B343D CRC64;
 01-0CT-2003 (TrEWBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Conserved hypothetical protein.
 Pred. No. 4.3e+02;
: Mismatches 0;
 152 AA.
 152 AA
 0; Mismatches
 PRT;
 PRT;
 100.0%;
 SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
 5; Conservative
 PRELIMINARY;
 5; Conservative
 PRELIMINARY;
Best Local Similarity
Matches 5; Conserv
 Local Similarity
 SEQUENCE FROM N.A.
 ||||||
56 SVIAK 60
 81 SVIAK 85
 1 SVIAK 5
 1 SVIAK 5
 NCBI_TaxID=1773;
 Query Match
 Q8VK36
 Q7U080
 RESULT 13
 Matches
 RESULT 14
 Q8VK36
 Q7U080
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 Gaps
 MEDLINE=20092464; PubMed=10628842;
Karch H., Schmidt H., Janetzki-Mittmann C., Scheef J., Kroeger M.;
"Shiga toxins even when different are encoded at identical positions in the genomes of related temperate bacteriophages.";
Mol. Gen. Genet. 262:600-607(1999).
BMBL; AJ237660; CAB39993.1; --
SEQUENCE 161 AA; 18497 MW; Al124675BE0F5896 CRC64;
 Gaps
 Bacteriophage 21.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
VCBI_TaxID=10743;
 0
 .,
 Length 152;
 Length 161;
 0; Indels
16626 MW; 60E64662DC2B343D CRC64;
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 1 100.0%; Score 21; DB 16; Similarity 100.0%; Pred. No. 4.6e+02; 5; Conservative 0; Mismatches 0;
 100.0%; Score 21; DB 9; I
100.0%; Pred. No. 4.9e+02;
ative 0; Mismatches 0;
 161 AA
 Search completed: August 12, 2004, 06:19:32 Job time : 13.5512 secs
 PRT;
 5; Conservative
 PRELIMINARY;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2004, 06:12:47; Search time 0.307377 Seconds (without alignments) 847.008 Million cell updates/sec Run on:

US-09-890-463-1 21 1 SVIAK 5 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched: 141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                | QBuaxO agrobacteri QBevvs mycoplasma QBty3 methanosarc QBywm7 methanosarc QBywm7 methanosarc QBywm7 methanosarc QByw25 staphylococ QDux89 staphylococ QDux89 staphylococ QDux89 staphylococ QDux89 staphylococ QDux80 herpes simp QBYB18 herpes simp QBYB18 herpes simp QBYB18 herpes simp QBYB18 herpes simp QBYB19 hermoplasm QBYB19 hermoplasm QBYB113 m dimethyla PBTF113 m dimethyla QBTF113 m dimethyla QBTF113 m dimension QBTF113 |
|----------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| SUMMARIES                  | MINE AGRIS RL27_MYCPE SR19_METAC SR19_METAC SR19_METAC SR19_METAC SR19_METAC SR19_METAC SR19_METAC SR3_TARW WR12_STRAW WR12_STRAW WR12_FRW WR3_THEVO RNH2_STRAW CYIL_HEVO! RNH2_STRAW CYIL_HEVO! RNH2_STRAW CYIL_HEVO! RNH2_STRAW WRS1_THEVO RNH2_STRAW WRS1_THEVO RNH2_STRAW WRS1_THEVO! WRS1_THEVO! MATA_NEUCR OYNI_HUMAN DPOB_HUMAN DPOB_HUMAN DPOB_HUMAN DPOB_HUMAN DPOB_HUMAN DPOB_HUMAN DPOB_HUMAN MUAI_THETN REBX_SALIY SAHH RALSO TEG_CANAL CANAL CANAL CANAL CANAL CANAL SAHIY SANIT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| DB                         | <br>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| %<br>Query<br>Match Length | 86<br>101<br>101<br>118<br>1188<br>1222<br>2224<br>2225<br>2225<br>2233<br>2233<br>2233<br>2233<br>2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| Score                      | 222222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Result<br>No.              | 1 1 2 2 2 4 4 8 8 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

| Q9ce12 lactococcus | P38788 saccharomyc | Q40545 nicotiana t | P22317 alcaligenes | Q11174 caenorhabdi | Q08759 xenopus lae | 076031 homo sapien | Q9jhs4 mus musculu | P06876 mus musculu | P46200 bos taurus | P10242 homo sapien | P01103 gallus gall |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
| SYR_LACLA          | YHM4 YEAST         | KPYA TOBAC         | HOXF ALCEU         | CHIT CAEEL         | MYB XENLA          | CLPX HUMAN         | CLPX_MOUSE         | MYB MOUSE          | MYB_BOVIN         | MYB_HUMAN          | MYB_CHICK          |
| H                  | н                  | H                  | Н                  | Н                  | Н                  | Н                  | Н                  | Н                  | Н                 | 1                  | Н                  |
| 564                | 572                | 593                | 602                | 617                | 624                | 633                | 634                | 636                | 640               | 640                | 641                |
| 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0             | 100.0              | 100.0              |
| 21                 | 21                 | 21                 | 21                 | 21                 | 21                 | 21                 | 21                 | 21                 | 21                | 21                 | 21                 |
| 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                | 44                 | 45                 |

## ALIGNMENTS

| SULT 1<br>NE AGRT5<br>MINE AGRT5<br>QBUAX0;<br>10-OCT-2003 |       | <pre>C Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium. K NCBI TaxID=176299; W [1]</pre> |     |     | A Okura V.K., Zhou Y., Chen L., Wood G.E., Aimelda W.F. Ji., Woo L., A Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., |     |    |     |          |            | ·  | N [2] |   |    |     |    |   | RT "Genome sequence of the plant pathogen and biotechnology agent<br>RT Agrobacterium tumefaciens CSB.": | Science 294:23 | CC -!- FUNCTION: Prevents the cell division inhibition by proteins minC | and with a Internal division at the proper site by polar sites. This ensures cell division at the proper site by |   | <pre>CC the long axis of the cell (By similarity).<br/>CC -!- SIMILARITY: Belongs to the minE family.</pre> |   |     | CC the Buropean Bioinformatics Institute. There are no restrictions on its | C modified and this statement in tremoved. Usage by and for commercial modified and this statement from the http://www.ish-sib.ch/announce/ | or send an email to license | )<br> |
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 Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
-!- SIMILARITY: Belongs to the L27P family of ribosomal proteins.
 Gaps
 Gaps
 Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 ..
 .
0
 100.0%; Score 21; DB 1; Length 86; 100.0%; Pred. No. 40; o; Indels ive 0; Mismatches 0; Indels
 100.0%; Score 21; DB 1; Length 95; 100.0%; Pred. No. 44;
 0; Indels
 735D951C94B7A730 CRC64;
 Cell division, Complete proteome.
SEQUENCE 86 AA, 9703 MW; B0E274F6A48D52F2 CRC64;
 Last sequence update)
Last annotation update)
 95 AA
 Mismatches
 PRINTS; PROD063; RIBOSOMALL27.
ProDom, PD003114; Ribosomal L27; 1.
TIGRFAMS, TIGRO062; L27; 1.
PROSITE; PS00831; RIBOSOMAL L27; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 95 AA; 10464 MW; 735D951
 HAMAP; MF 00539; -; 1.
InterPro; IPR001684; Ribosomal L27.
Pfam; PF01016; Ribosomal L27; I.
 MEDLINE=22354719; PubMed=12466555;
 100.08; Pt. 100.08;
EMBL; AE009254; AAL44663.1; --
BNBL; ABC08359; AAK90142.1; --
PIR; AL2955; A12955.
PIR; D98327; D98327.
IMPANAP; MF_00262; -; I.
InterPro; IPR005527; Minb.
Pfam; PF03776; Minb.
 15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last seq
15-MAR-2004 (Rel. 43, Last ann
 EMBL; AP004171; BAC44234.1; -.
 TIGRFAMS; TIGR01215; minE; 1.
 Query Match
Best Local Similarity 100.v.
 50S ribosomal protein L27.
 STANDARD;
 Conservative
 Query Match
Best Local Similarity
Lac 5; Conserv
 SEQUENCE FROM N.A.
 45 SVIAK 49
 NCBI_TaxID=28227;
 1 SVIAK 5
 RPMA OR MYPE4440
 STRAIN=HF-2
 MYCPE
 QBEVWS;
 RESULT 2
RL27 MYCPE
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91 SVIAK 95

RESULT 3 SR19\_METAC

1 SVIAK 5

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MEDINE-21929760; PubMed=1193238;

MEDINE-21929760; PubMed=1193238;

Galagan J.E., Nubbaum C., Roy A., Endrizzi M.G., Macdonald P.,

Galagan J.E., Nubbaum C., Roy A., Endrizzi M.G., Macdonald P.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Allen N., Naylor J., Grann I., Graham D.E., Graham D.A., Graham D.A.,

Allen N., Burber R.D., Cann I., Graham D.B., Graham D.A.,

Allederich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Aledy J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Aledy J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Apringer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

Pritchett W.W., Birren B.,

The genome of Methanosarcina acetivorans reveals extensive metabolic

and physiological diversity, ",

Genome Res. 12:532-542(2002).

I. FUNCTION Signal-recognition-particle assembly, binds directly to
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 -!- SUBUNIT: Archaeal signal recognition particle consists of a 75 RNA molecule of 300 nucleotides and two protein subunits: SRP54 and
 Gaps
 .
0
 Signal recognition particle; RNA-binding; Ribonucleoprotein; Complete proteome SEQUENCE 101 AA; 11415 MW. 8DA2R11AAA9650AA7
 Methanosarcina acetivorans.
Archaea; Buryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
 100.0%; Score 21; DB 1; Length 101; 100.0%; Pred. No. 46;
 0; Indels
 SRP19 (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the SRP19 family.
 101 AA; 11415 MW; 8DA2E31AAA9594C3 CRC64;
 28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Signal recognition particle 19 kDa protein (SRP19).
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Signal recognition particle 19 kDa protein (SRP19).
SRP19 OR MM1557.
 Mismatches
 EMBL; AE010688; AAM03745.1; ALT_INIT.
 0;
28-FEB-2003 (Rel. 41, Created)
 HAMAP; MF_00305; -; 1.
InterPro; IPR002778; SRP19.
 Pfam; PF01922; SRP19; 1.
ProDom; PD006609; SRP19; 1.
 5; Conservative
 STANDARD;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 79 SVIAK 83
 NCBI_TaxID=2214;
 SRP19 OR MA0292.
 . 1 SVIAK 5
 similarity).
 SR19 METMA
 Q8PWM7;
 RESULT 4
SR19_METMA
 GERARA
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L5-MAR-2004
 PUR3 STAAM
 TRANSMEM
TRANSMEM
SEQUENCE
 Query Match
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 PUR3_STĂAM
 Matches
 RESULT 6
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 ò
 -1- SUBUNIT: Archaeal signal recognition particle consists of a 78 RNA molecule of 300 nucleotides and two protein subunits: SRP54 and SRP19 (By similarity).
-!- SUBCELLULAR LOCATION: 2. SUBCELLULAR LOCATION: 0. SUBCELLULAR LOCATION to the SRP19 family.
 Deppenment U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
Bruegagemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
Fritz H.-J., Gottschalk G.,
"The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea.",
J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
-!- FUNCTION: Signal-recognition-particle assembly, binds directly to
 Gaps
 STRAIN=Rd / KW20 / ATCC 51907;
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95550630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,
 .
 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
 Signal recognition particle; RNA-binding; Ribonucleoprotein;
Methanosarcina mazei (Methanosarcina frisia).
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
 Length 101;
 0; Indels
 101 AA; 11377 MW; 3F9235C41CF68C74 CRC64;
 SEQUENCE FROM N.A.
STRAIN-GOel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
MEDLINE-22120827; PubMed=12125824;
 100.0%; Score 21; DB 1; 100.0%; Pred. No. 46;
 Q574<u>Z5; P96638;</u>
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 134 AA
 0; Mismatches
 PRT;
 EMBL; AE013390; AAM31253.1; -.
 Hypothetical protein HI1077.1
 HAMAD; MF 00305; -; 1.
InterPro; IPR002778; SRP19.
Pfam; PF01922; SRP19; 1.
 ProDom; PD006609; SRP19; 1
 5; Conservative
 STANDARD;
 Haemophilus influenzae.
 Best Local Similarity
 Complete proteome. SEQUENCE 101 AA;
 SVIAK 83
 1 SVIAK 5
 NCBI_TaxID=2209;
 similarity).
 YA7B HAEIN
 79
 Query Match
 HI1077.1
 Matches
```

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 "Whole-genome random sequencing and assembly of Haemophilus influenzae
 Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Acki K.-I., Nagai Y., Lian J.-C., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashitea A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K., Yoshino C., Shiba T.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
 -:- CATALYTIC ACTIVITY: 10-formyltetrahydrofolate + N(1) - (5-phospho-D-ribosyl)glycinamide = tetrahydrofolate + N(2) - formyl-N(1) - (5-phospho-D-ribosyl)glycinamide.
-!- PATHWAY: De novo plurine biosynthesis; third step.
-!- SUBUNT: Homodimer (By similarity).
-!- SUBUNT: Homodimer (By similarity).
 Gaps
 (EC 2.1.2.2) (GART) (GAR
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.
 Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: WEAK, TO BACTERIAL PNUC PROTEINS.
 Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.,
 0;
 15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (GART'
transformylase) (5'-phosphoribosylglycinamide transformylase).
PURN OR SAV1072 OR SA0924.
 100.0%; Score 21; DB 1; Length 134; 100.0%; Pred. No. 60;
 0; Indels
 Pfam; PF04973; NMN transporter; 1.
TIGREMS: TIGR01528; NMN trans PnuC; 1.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 23 43 POTENTIAL.
 70C1620F88D0E6BF CRC64;
 Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879;
 188 AA
 0; Mismatches
 POTENTIAL. POTENTIAL.
 SEQUENCE FROM N.A.
STRAIN=Mu50 / ATCC 700699, and N315;
MEDLINE=21311952; Pubmed=11418146;
 InterPro; IPR006419; NMN_trans PnuC.
 PRT;
 (Rel. 43, Created)
 134 AA; 14415 MW;
 EMBL; U32788; AAC22744.1; -.
TIGR; H11077.1; -.
 Lancet 357:1225-1240(2001)
 5; Conservative
 STANDARD;
 Local Similarity
 75 SVIAK 79
 1 SVIAK 5
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 .
0
 Lancet 359:1819-1827(2002).

-!- CATALYTIC ACTIVITY: 10-formyltetrahydrofolate + N(1)-(5-phospho-D-ribosyl)glycinamide = tetrahydrofolate + N(2)-formyl-N(1)-(5-phospho-D-ribosyl)glycinamide.
-!- PATHWAY: Do novo purine biosynthesis; third step.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBUNIT: Homodimer (By similarity).
 15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (GART) (GAR transformylase) (5'-phosphoribosylglycinamide transformylase).
 Gaps
 MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
T., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
 .,
 Score 21; DB 1; Length 188; Pred. No. 82;
 0; Indels
 D034134258D89AEE CRC64;
 EMB1; AFUUJAISE,
PIR; F89876; F89876.
HSSP: P08179; 10AR.
SWISS-2DPAGE; Q99V25; STAAN.
INTERPEVO; IPRO02376; formyl transf.
Pfam; PF00551; formyl transf; 1.
PROSITE; PS00373; GART; FALSE_NEG.
Purine blosynthesis; Transferase; Complete proteome.
146 BY SMILARITY.
 F0364618F275FA30 CRC64;
 InterPro; IPR002376; formyl transf.

Pfam; PF00551; formyl transf; 1.

PROSITE; PS03373; GART; FALSE NEG
PURITE blosynthesis; Transferase; Complete proteome.

ACT SITE 146

BY SIMILARITY.

SEQÜENCE 188 AA; 21153 MW; D034134258D89AEE CRC6
 Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes; Bacillales; Staphylococcus.
 188 AA
 0; Mismatches
 EMBL; AP003361; BAB57234.1; -. EMBL; AP003132; BAB42169.1; -.
 100.0%;
 EMBL; AP004825; BAB94820.1; -.
 Lancet 359:1819-1827(2002)
 Query Match
Best Local Similarity 100.
The Si Conservative
 STANDARD;
 NCBI_TaxID=196620;
 181 SVIAK 185
 SEQUENCE FROM N.A.
 1 SVIAK 5
 acquired MRSA."
 PURN OR MW0955.
 STAAW
 OBNXB9;
 PUR3_STAAW
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 0
 0
 -!- FUNCTION: This enzyme is an endonuclease that degrades the RNA of RNA-DNA hybrids specifically (By similarity).
 SEQUENCE FROM N.A.
MEDLINE-2285697, PubMed=12917641;
MEDLINE-2285697, PubMed=12917641;
Palentik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,
Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
Dufresene A., Partensky F., Webb E.A., Waterbury J.;
"The genome of a mottle marine Synechococcus.";
Nature 424:1037-1042(2003)
 Gaps
 Gaps
 ..
 0;
 100.0%; Score 21; DB 1; Length 224; 100.0%; Pred. No. 96;
100.0%; Score 21; DB 1; Length 188; 100.0%; Pred. No. 82;
 Indels
 Indels
 RNHB OR SYNW2144.
Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
NCBI_TaxID=84588;
 phosphomonoester.
-!- COFACTOR: Manganese (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the RNase HII family.
 0
 0
 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Latt sequence update)
01-PAR-2004 (Rel. 43, Last annotation update)
Glycoprotein L precursor.
 (Rel. 43, Created)
(Rel. 43, Last sequence update)
(Rel. 43, Last annotation update)
HII (EC 3.1.26.4) (RNase HII).
 224 AA
 Mismatches
 0; Mismatches
 EMBL; BX569694; CAE08659.1; ALT_INIT.
 HAMAP; MF 00052; -; 1.
InterPro; IPR001352; RNase HII/HIII.
Pfam; PF01351; RNase HII; 1.
 100.0%; FIL
 5; Conservative
 STANDARD;
 5; Conservative
 STANDARD;
 Best Local Similarity
 167 SVIAK 171
 Best Local Similarity
 181 SVIAK 185
 1 SVIAK 5
 Ribonuclease HII
 1 SVIAK 5
 L5-MAR-2004
 15-MAR-2004
15-MAR-2004
 VGLL HSV2H
P28278;
 SYNPX
 Query Match
 Query Match
 RESULT 9
VGLL_HSV2H
 RESULT 8
RNH2_SYNPX
 Matches
 Matches
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24726 MW;
 EMBL; AL445067; CAC12389.1; -
 Ouery Match
Best Local Similarity 100.۰
است 5; Conservative
 STANDARD;
 SEQUENCE 225 AA;
 92 SVIAK 96
 1 SVIAK 5
 similarity)
 RS3 THEVO
 097EX1;
 RS3_THEVO
SO DE REPORTE DE LA COCCOCIO DEL LA COCCOCIO DE LA COCCIO DE LA COCIO DE LA COCCIO DE LA COCCIO DE LA COCCIO DE LA COCCIO DE LA COCI
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 ;
0
 Gaps
 Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
 SEQUENCE FROM N.A.
MEDIATE=9213549; bubMed=1662697;
MEDIATE=9213549; bubMed=1662697;
"Comparative sequence analysis of the long repeat regions and adjoining parts of the long unique regions in the genomes of herpes simplex viruses types 1 and 2.";
J. Gen. Virol. 72:3057-3075(1991).
 -!- FUNCTION: ASSOCIATED WITH GLYCOPROTEIN H (GH) TO FORM A COMPLEX IMPORTANT FOR INFECTION AND CELL FUSION (BY SIMILARITY).
 N-LINKED (GLCNAC. . .) (POTENTIAL)
CD585849250D7C1F CRC64;
 .
0
 Nature 407:508-513(2000).
-!- FUNCTION: Binds the lower part of the 30S subunit head (By
 Length 224;
 Archaea; Euryarchaecta; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
 0; Indels
 Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
 Herpes simplex virus (type 2 / strain HG52).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
 100.0%; Score 21; DB 1; 100.0%; Pred. No. 96;
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Solosomal protein S3P.
RPS3P OR TA1265.
 GLYCOPROTEIN L.
 225 AA
 0; Mismatches
 POTENTIAL.
 PRT;
 MEDLINE=20479972; PubMed=11029001;
 EMBL, D10470; BAA01264.1; -.
EMBL, 286099; CAB06761.1; -.
EMIL, JQ1494; WMBEHG.
InterPro; IRR007923; Herpes ULI.
Pfam; PF05259; Herpes_ULI.
 25192 MW;
 5; Conservative
 Thermoplasma acidophilum.
 STANDARD;
 16
224
 Glycoprotein; Signal.
SIGNAL 1
 224 AA;
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SVIAK 34
 NCBI_TaxID=10315;
 STRAIN-DSM 1728;
 1 SVIAK 5
 NCBI_TaxID=2303;
 similarity)
 acidophilum."
 RS3 THEAC
 Dolan A.;
 CARBOHYD
 SEQUENCE
 Query Match
 Q9HIRS;
 Matches
δ
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 0
 Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T., Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.; Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium."r Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262 (2000).
 Gaps
-!- SUBUNIT: Part of the 30S ribosomal subunit.
-!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
 Pfam; PF00013; KH; 1.

Pfam; PF00189; Ribosomal_S3_C; 1.

PARAT; SM00322; KH; 1.

PROSITE; PS50823; KH TYPE_2; 1.

PROSITE; PS00548; RIBOSOWAL S3; FALSE NEG.

Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome. DOMAIN
 -!- SUBUNIT: Part of the 30S ribosomal subunit.
-!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
-!- SIMILARITY: Contains 1 KH type-2 domain.
 0
 100.0%; Score 21; DB 1; Length 225; 100.0%; Pred. No. 97;
 Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
NCBI_TaxID=50339;
 0; Indels
 FE2B2B220091017F CRC64;
 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sols ribosomal protein S3P.
RPS3P OR TV0334 OR TVG0336522.
 0; Mismatches
 or send an email to license@isb-sib.ch).
 . 83 C.
 SEQUENCE FROM N.A.
STRAIN=GSS1 / DSM 4299 / JCM 9571;
MEDLINE=20570466; PubMed=11121031;
 HAMAP; MF_01309; -; 1.
InterPro; IPR004087; KH_dom.
InterPro; IPR0040819; KH_Brok.
InterPro; IPR004044; KH_TYPE_2.
InterPro; IPR001311; Ribosomal_S3
InterPro; IPR005703; S3_euk_arch.
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FLGD BUCAI
 RESULT 14
VNST_PTPV
 Matches
 RESULT 13
 DP
 SOUR SECOND STANDARY SERVICE S
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 ..
 R EMBL; Arcocci;

R HAMAP; MF 01309; -; 1.

R HAMAP; MF 01309; KH dom.

R InterPro; IPR004087; KH dom.

DR InterPro; IPR004049; KH TYPE C.

DR InterPro; IPR001031; Ribosomal_S3_C.

DR InterPro; IPR001351; Ribosomal_S3_C.

DR Pfam; PF00109; Ribosomal_S3_C; 1.

DR Pfam; PF00109; Ribosomal_S3_C; 1.

DR PROSTIE; PS00322; KH; 1.

DR PROSTIE; PS00548; RIBOSOMAL_S3; FALSE NEG.

RW RIDOSOMAL S3 FALSE NEG.

KW Ribosomal protein; RNA-binding; rRNA-binding; RNA-binding; rRNA-binding; RNA-binding; RNA-bind
 -I-FUNCTION: This enzyme is an endonuclease that degrades the RNA of RNA-DNA hybrids specifically (By similarity).
 Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
 Gaps
 "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
 .
0
 SEQUENCE FROM N.A.

STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

STRAIN=21477403; PubMed=11572948;

Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.;

Wenome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
 Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Length 225;
 0; Indels
 SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRL 8165;
MEDLINE=22608306; PubMed=12692562;
 Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 phosphomonoester.
COFACTOR: Manganese (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: Belongs to the RNase HII family.
 Streptomycineae; Streptomycetaceae; Streptomyces.
 100.0%; Score 21; DB 1; 100.0%; Pred. No. 97;
 IS-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
115-MAR-2004 (Rel. 43, Last annotation update)
RIMHB OR RNH OR SAV2453.
 233 AA.
 0; Mismatches
 send an email to license@isb-sib.ch)
 EMBL; AP000992; BAB59476.1; -.
 STANDARD;
 SVIAK 96
 1 SVIAK 5
 RNH2 STRAW
 282KF0;
g
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and for commercial
 (See http://www.isb-sib.ch/announce,
 Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 Gaps
 Gaps
 Buchnera sp. APS.";
Nature 407:81-86(2000).
-!- FUNCTION: REQUIRED FOR FLAGELLAR HOOK FORMATION. MAY ACT AS A SCAFFOLDING PROTEIN (BY SIMILARITY).
 STRAIN=TOkyo 1998;
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 EMBL; AP005030; BAC70164.1; -.
HAMAP; MF 00052; -; 1.
InterPro: 1PR01352; RNase HII/HIII.
Fém.; PP01351; RNase HII; I.
Hydrolase; Nuclease; Endonuclease; Manganese; Complete proteome.
ACT SITE 27 27 BY SIMILARITY.
ACT SITE 139 BY SIMILARITY.
ACT SITE 138 138 BY SIMILARITY.
SEQUENCE 233 AA; 25206 MW; ADD09E96316IFE19 CRC64;
 ;
 ·.
 100.0%; Score 21; DB 1; Length 233; 100.0%; Pred. No. 1e+02;
 100.0%; Score 21; DB 1; Length 236; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
 Indels
рλ
 EMBL, AP001119; BAB13044.1; -.
InterPro; IPR005648; FlgD.
Pfam; PF03963; FlgD; Flgp:
Flagellum; Complete proteome.
SEQUENCE 236 AA; 26187 MW; E15EAA2D3D84F293 CRC64;
 Usage
 0
 16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Basal-body rod modification protein flgD.
modified and this statement is not removed.
 236 AA
 0; Mismatches
 0; Mismatches
 entities requires a license agreement (S. or send an email to license@isb-sib.ch).
 16-OCT-2001 (Rel. 40, Created)
 Enterobacteriaceae; Buchnera.
 Best_Local Similarity 100.
Matches 5; Conservative
 Local Similarity 100.
nes 5, Conservative
 STANDARD;
 symbiotic bacterium)
 148 SVIAK 152
 NCBI_TaxID=118099;
 186 SVIAK 190
 SEQUENCE FROM N.A.
 1 SVIAK 5
 1 SVIAK 5
 FLGD OR BÛ339
 FLGD_BUCAI
 Query Match
 Query Match
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Search completed: August 12, 2004, 06:20:04
 Job time : 4.30738 secs
 TRANSMEM
 TRANSMEM
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 Matches
SOUR SERVICE S
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 ;
0
 -:- MISCELLANEOUS: This protein may be a transcriptase component.
-:- SIMILARITY: NS-S FROM PUNTA TORO, RIFT VALLEY FEVER, SANDFLY FEVER SICILIAN, TOSCANA, AND UUKUNIEMI VIRUSES ARE EVOLUTIONARY RELATED.
 SEQUENCE FROM N.A.
STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
MEDLINE=22022145; PubMed=12024217;
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Berrollini M.C., Camargo L.E.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapbina L.P.,
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
 Gaps
 MEDLINE=84276006; PubMed=6087547;
Ihara T., Akashi H., Bishop D.H.L.;
"Novel coding strategy (ambisense genomic RNA) revealed by sequence analyses of Punca toro phlebovirus S RNA.";
Virology 136:293-306(1984).
 Wiggerich H.G., Klauke B., Koeplin R., Priefer U.B., Puehler A.; "Unusual structure of the tonB-exb DNA region of Kanthomonas campestris pv. campestris: tonB, exbB, and exbD1 are essential for ferric iron uptake, but exbD2 is not."; J. Bacteriol. 179:7103-7110(1997).
 Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
 Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 ..
 Length 250;
 0; Indels
 Nonstructural protein; Transcription.
SEQUENCE 250 AA; 29097 MW; 2C8909AlEDAD90D7 CRC64;
 100.0%; Score 21; DB 1; L
100.0%; Pred. No. 1.1e+02;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Nonstructural protein NS-S.
Punta toro phlebovirus.
 (Rel. 41, Last sequence update) (Rel. 41, Last annotation update)
 250 AA
 0; Mismatches
 or send an email to license@isb-sib.ch).
 Biopolymer transport exbB protein. EXBB OR XCC0009.
 PRT;
 MEDLINE=98037510; PubMed=9371459;
 15-DEC-1998 (Rel. 37, Created)
 Kanthomonadaceae; Xanthomonas
 EMBL; K02736; AAA47115.1; -.
 Local Similarity 100.
 STANDARD;
 STANDARD;
 PIR; A04108; MNVUPT.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 55 SVIAK 59
 1 SVIAK 5
 NCBI_TaxID=11587
 NCBI_TaxID=340;
 28-FEB-2003
 EXBB XANCP
034260;
 STRAIN=B100
 VNST PTPV
P03516;
 Query Match
 EXBB XANCP
 RESULT 15
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F., Locali B.C., Machado M.A., Madelra A.M.B.N., Martinez-Rossi N.N., Martins E.C., Maidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Secubal J.C., Kitajima J.P., Comparison of the genomes of two Xanthomonas pathogens with differing
 -!- FUNCTION: Involved in the tonB-dependent energy-dependent transport of various receptor-bound substrates. Protects exbD from proteolytic degradation and functionally stabilizes tonB (By
 Gaps
 -!- SUBBUILT: The accessory proteins exbB and exbD seem to form a complex with tonB (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: Belongs to the exbB / tolQ family.
 ..
 Pfam; PF01618; MotA ExbB; 1.
Transport; Protein transport; Transmembrane; Inner membrane;
 Score 21; DB 1; Length 253;
Pred. No. 1.1e+02;
 Indels
 90138F91BC714508 CRC64;
 0
 A -> R (IN REF. 1).
 100.0%; Pred. wo.
 POTENTIAL. POTENTIAL.
 POTENTIAL.
 EMBL; AE012094; AAM39328.1; -. InterPro; IPR002898; MotA_ExbB.
 26666 MW;
 100.08;
 EMBL; Z95386; CAB08609.1; -.
 host specificities.";
Nature 417:459-463(2002).
 5; Conservative
 204 2
114 1
253 AA;
 Query Match
Best Local Similarity
 Complete proteome.
 230 SVIAK 234
 1 SVIAK 5
 similarity).
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

August 12, 2004, 06:12:47; Search time 0.461066 Seconds (without alignments) 1043.144 Million cell updates/sec Run on:

US-09-890-463-1 21 1 SVIAK 5 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| S  | 221<br>21<br>21 | 2년   6666 | Length<br>86<br>132<br>171 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | ID<br>A12955<br>A12957<br>T32273<br>G90532 | Description cell division topo cell division topo hypothetical prote hypothetical prote |
|----|-----------------|-----------|----------------------------|---------------------------------------|--------------------------------------------|-----------------------------------------------------------------------------------------|
| 21 |                 | 100.0     | 181                        | 0 0                                   | AF1931<br>F89876                           | hypothetical prote<br>phosphoribosylglyc                                                |
| 21 |                 | 100.0     | 194                        | 0 0                                   | T15115<br>D87309                           | hypothetical prote<br>hypothetical prote                                                |
| 21 |                 | 100.0     | 200                        | 20                                    | AG1137                                     | probable sugar-pho                                                                      |
| 21 |                 |           | 203                        | 4 (7                                  | - n                                        | hypothetical prote                                                                      |
| 21 |                 | 100.0     | 219                        | N                                     | A97665                                     | tetR family bacter                                                                      |
| 21 |                 | 100.0     | 219                        | Ν,                                    | AD2889                                     | scription                                                                               |
| 27 |                 | 100.0     | 224                        | ٦ ،                                   | WMBEHG<br>D84969                           | basal-body rod mod                                                                      |
| 21 |                 |           | 243                        | 1 7                                   | H95909                                     | probable membrane-                                                                      |
| 21 |                 | 100.0     | 250                        | Н                                     | MNVUPT                                     | nonstructural prot                                                                      |
| 21 |                 | 100.0     | 263                        | Н                                     | S73489                                     | probable S-adenosy                                                                      |
| 21 |                 | ٦.        | 266                        | N                                     | G81674                                     |                                                                                         |
| 21 | ,               | 100.0     | 268                        | 7                                     | D64217                                     | ribosomal protein                                                                       |
| 23 |                 | 100.0     | 271                        | ٦                                     | ELRT2                                      | pancreatic elastas                                                                      |
| 2  | _,              |           | 279                        | ~                                     | T50125                                     | -acylg                                                                                  |
| 2  |                 | 100.0     | 282                        | Н                                     | JQ0347                                     | cytochrome c1 - Rh                                                                      |
| 21 |                 | 100.0     | 293                        | ~                                     | 865582                                     | mating type protei                                                                      |
| 21 |                 | 00        | 301                        | 7                                     | A95910                                     | probable glycosylt                                                                      |
| 21 |                 |           | 305                        | N                                     | H82684                                     | acetyltransferase                                                                       |
| 21 |                 | 00.       | 331                        | 7                                     | F97767                                     | hypothetical prote                                                                      |
| 21 |                 | 100.0     | 335                        | 7                                     | S48061                                     |                                                                                         |
| 21 |                 | 00        | 335                        | ď                                     | _                                          | DNA-directed DNA p                                                                      |
|    |                 |           |                            |                                       |                                            |                                                                                         |

| aquaporin 9 - huma | early switch prote | probable hexosyltr | probable dloxygena | probable MYB tamil | hypothetical prote | hypothetical prote | early switch prote | hypothetical prote | hypothetical prote | early switch prote | hypothetical prote | hypothetical prote | hypothetical prote | hypothetical prote |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| JC5791             | A55473             | G69290             | C84713             | T01017             | B96601             | T49186             | B55473             | A96601             | AF2464             | C55473             | S15308             | G85877             | F91033             | T30092             |
| (1)                | v H                | Н                  | ~                  | 0                  | N                  | 7                  | 0                  | ~                  | ď                  | 7                  | N                  | 7                  | 7                  | 7                  |
| 342                | 355                | 357                | 358                | 367                | 396                | 399                | 417                | 418                | 420                | 426                | 430                | 470                | 470                | 498                |
| 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              | 100.0              |
| 21                 | 21                 | 21                 | 21                 | 21                 | 21                 | 27                 | 21                 | 21                 | 21                 | 21                 | 21                 | 21                 | 21                 | 21                 |
| 30                 | 31<br>32           | 33                 | 34                 | 35                 | 36                 | 3.7                | 38                 | 36                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

### ALIGNMENTS

# RESULT 2

division topological specificity factor [imported] - Agrobacterium tumefaciens (stress) division topological specificity factor [imported] - Agrobacterium tumefaciens (stress) dispecies: Agrobacterium tumefaciens (species: Agrobacterium tumefaciens (species: Agrobacterium tumefaciens (species: Agrobacterium tumefaciens) dispecies: Agrobacterium tumefaciens (species: Agricultum) dispecience (species: Agricultum) dispecies: Agricultum) dispecies: Agricultum dispecies: Agr

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-86 <KUR>

A;Cross-references: GB:AE007870; PIDN:AAK90142.1; PID:g15160139; GSPDB:GN00170 C;Genetics: A;Gene: AGR L 3134 A;Map position: linear chromosome

·

```
C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. ptc 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AF1931

S;Kaneko, T.; Nakamura, Y.; Wollk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, S. DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
 phosphoribosylglycinamide formyltransferase [imported] - Staphylococcus aureus (strain N C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 21-Jun-2002
C;Accession: F89876
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc C.; Shiba, T.; Hattcri, M.; Obayashi, N.; Awano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Lancet, 357, 1225-1240, 2001
 A;Residues: 1-194 <BRA>
A;Cross-references: EMBL:AF014939; NID:g2275620; PID:g2275628; PIDN:AAB63931.1; GSPDB:GN
A;Experimental source: strain Bristol N2; clone ZC132
 A;Residues: 1-181 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB72958.1; PID:917130347; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
 A;Residues: 1-188 «KUR»
A;Cross-references: GB:BA000018; PID:g13700873; PIDN:BAB42169.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
 A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146 A,Accession: F89876
 hypothetical protein ZC132.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15115, K. Stradshaw, H.; Devlin, K. submitted to the EMBL Data Library, July 1997 A;Description: The sequence of C. elegans cosmid ZC132.
 Gaps
 Gaps
 ..
0
 ..
0
 100.0%; Score 21; DB 2; Length 181; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
 Length 188;
 0; Indels
 h
Similarity 100.0%; Score 21; DB 2; I
Similarity 100.0%; Pred. No. 1.2e+02;
5; Conservative 0; Mismatches 0;
 A,Accession: T15115
A,Status: preliminary; translated from GB/EMBL/DDBJ
 5; Conservative
 A; Reference number: Z18294
 Best Local Similarity
Matches 5; Conserv
 Query Match
Best Local Similarity
 181 SVIAK 185
 37 SVIAK 41
 A;Status: preliminary A;Molecule type: DNA
 1 SVIAK 5
 A, Status: preliminary A, Molecule type: DNA
 1 SVIAK 5
 A; Molecule type: DNA
 A; Gene: alr1001
 Query Match
 Matches
 à
 à
 d
 hypothetical protein MYPU 1670 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C.Species: Mycoplasma pulmonis
C.Becies: Mycoplasma pulmonis
R.Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
R.Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
A.Ttle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A.Reference number: A99512; MUID:21267165; PMID:11353084
A.Recession: G90532
A.Recession: G90532
A.Residues: I-171 <KUR.
A.Residues: I-171 <KUR.
A.Residues: GB:AL445566; PID:914089580; PIDN:CAC13340.1; GSFDB:GN00153
A.Experimental source: strain UAB CTIP
A.Genetic code: SGC3
 C; Juace: zy-oct-luyy #sequence_revision zy-Oct-luyy #text_cnange vy-oun-zvou C; Accession: T33373
R; Scheet, P.; Maggi, L.
R; Scheet, P.; Maggi, L.
A; Description: The sequence of C. elegans cosmid COIB12.
A; Description: The sequence of C. elegans cosmid COIB12.
A; Reference number: 221156
A; Reference number: 22156
A; Residues: 1-132 A; SCH3
A; Residues: CSPS: COIB12.
A; Residues: CSPS: COIB12.
A; Reperimental source: strain Bristol N2; clone COIB12
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Color Cibil
 ö
 0
 ;
 Species: Caenorhabditis elegans
Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
 Gaps
 Gaps
 Gaps
 AF1931
hypothetical protein alr1001 [imported] - Nostoc sp. (strain PCC 7120)
 ·,
 .
0
 .;
0
 h Similarity 100.0%; Score 21; DB 2; Length 132; Similarity 100.0%; Pred. No. 86; 5; Conservative 0; Mismatches 0; Indels
 100.0%; Score 21; DB 2; Length 171; larity 100.0%; Pred. No. 1.1e+02; Conservative 0; Mismatches 0; Indels
 Query Match
Best Local Similarity 100.0%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 0; Indels
 hypothetical protein C01B12.7 - Caenorhabditis elegans
 Best_Local Similarity
Matches 5; Conserv
 Query Match
Best Local Similarity
Matches 5; Conserv
 45 SVIAK 49
 117 SVIAK 121
 25 SVIAK 29
 1 SVIAK 5
 1 SVIAK 5
 1 SVIAK 5
 Query Match
```

à g 0

RESULT 5

ო

A;Gene: CESP:ZC132.9 A;Map position: 5 A;Introns: 135/3; 153/3

C; Genetics:

56 SVIAK 60

qq

RESULT 8

1 SVIAK 5

```
hypothetical protein F13M23.120 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Appr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05519
R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.)
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15419
A;Accession: T05519
 Cispecies: Agrobacterium tumefaciens
Cispecies: Agrobacterium tumefaciens
Cispecies: Agrobacterium tumefaciens
Cispecies: Agrobacterium tumefaciens
Cispecies: Agrobacterium tumefaciens
Cispecies: Agrobacterium tumefaciens
Cispecies: Agrobacterium tumefaciens
Cispecies: Agrobacterium tumefaciens
Richard B.; Minkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Litle Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A; Reference number: A97359; MUID:21608551; PMID:11743194
 The Cold Spring
 hypothetical protein AT4924980 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C; Accession: C85288 R; Anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Colonature 402, 769-777, 1999 A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A; Reference number: A85001; MUID:20083488; PMID:10617198
 0,
 ö
 A;Residues: 1-203 <STO>
A;Cross-references: GB:NC_001268; NID:g7269348; PIDN:CAB79407.1; GSPDB:GN00140
 Gaps
 Gaps
 0;
 ..
 Length 203;
 Length 203;
 Indels
 A;Cross-references: EMBL:AL035523
A;Experimental source: cultivar Columbia; BAC clone F13M23
C;Genetics:
 100.0%; Score 21; DB 2; I 100.0%; Pred. No. 1.3e+02;
 100.0%; Score 21; DB 2; I 100.0%; Pred. No. 1.3e+02;
 0; Mismatches
 0; Mismatches
 A, Note: intron positions not resolved A, Note: F13M23.120
 5; Conservative
 5; Conservative
 Best Local Similarity
 Query Match
Best Local Similarity
Matches 5; Conserv
 A;Molecule type: DNA
A;Residues: 1-203 <BEV>
130 SVIAK 134
 30 SVIAK 34
 30 SVIAK 34
 1 SVIAK 5
 A,Accession: A97665
A,Status: preliminary
A,Molecule type: DNA
 1 SVIAK 5
 A;Status: preliminary
A;Molecule type: DNA
 A, Map position: 4
 A, Gene: AT4g24980
A, Map position: 4
 Query Match
 C; Genetics:
 RESULT 11
T05519
 Matches
 RESULT 12
 à
 g
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 C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG1137
C;Accession: AG1137
C;Accession: AG1137
C;Accession: AG1137
C;Accession: A.; Baquero, F.; Bloecker
C;Accession: AG1137
C;Accession: A.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mayauthors: Kreft, J.; Kuhn, M.; Tarerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
 Cipecies: Caulobacter crescentus
Cipacies: Caulobacter crescentus
Cipacies: Caulobacter crescentus
Cipacies: Caulobacter crescentus
Cipacies: On-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Dec-2002
Cipacession. B03309
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ernalaeva, M.; White, O.; Salzbact, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-414, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Status: preliminary
 probable sugar-phosphate isomerase homolog lmo0502 [imported] - Listeria monocytogenes
 A;Residues: 1-200 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC98581.1; PID:g16409878; GSPDB:GN00177
 0
 ·,
 6
 A; Cross-references: GB: AE005673; NID: 913421662; PIDN: AAK22472.1; GSPDB: GN00148
 Gaps
 Gaps
 Gaps
 .
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0
 ;
0
 Query Match

100.0%; Score 21; DB 2; Length 200;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels
 Length 194;
 Length 197;
 hypothetical protein CC0485 [imported] - Caulobacter crescentus
 0; Indels
 0; Indels
 100.0%; Score 21; DB 2; 1
100.0%; Pred. No. 1.38+02;
iive 0; Mismatches 0;
 100.0%; Score 21; DB 2; I 100.0%; Pred. No. 1.3e+02;
 Mismatches
 C; Superfamily: 508 ribosomal protein L25
 ·
0
 A; Experimental source: strain EGD-e
 Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
 Query Match
Best Local Similarity 100.
Matches 5; Conservative
```

A;Molecule type: DNA A;Residues: 1-197 <STO>

CC0485

C;Genetics:

SVIAK 77

73

RESULT 9

A;Status: preliminary A;Molecule type: DNA

A; Gene: 1mo0502

Genetics:

1 SVIAK 5

1 SVIAK 5

ð

```
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: D84969
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A.Reference number: A84930; MUID:20445173; PMID:10993077
 basal-body rod modification protein flgD [imported] - Buchnera sp. (strain APS)
 100.0%; Score 21; DB 2; Length 236; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
 A/Accession: D84969
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-236 <870>
A/Cross-references: GB:AP000398; GSPDB:GN00144
A/Experimental source: strain APS
C/Genetics:
A/Gene: flgD; BU339
 Search completed: August 12, 2004, 06:13:48 Job time : 3.46107 secs
 5; Conservative
 Query Match
Best Local Similarity
Matches 5; Conserv
 186 SVIAK 190
 30 SVIAK 34
 1 SVIAK 5
 엄
 g
 à
 C;Accession: AD2889
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell : Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AD2899
A;Reference number: AD2899
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <KUR>
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Cross-references: GB:AE008688; PIDN:AAL43530.1; PID:G17741041; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
 RESULT 14
WMBERG
ULI protein - human herpesvirus 2 (strain HG52)
C;Species: human herpesvirus 2
C;Species: human herpesvirus 2
A;Note: host Homo sapiens (man)
C;Date: all-bc-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jun-2000
C;Accession: J01494
R;McGeoch, D.J; Cunningham, C; McIntyre, G; Dolan, A.
J. Gen. Virol. 72, 3057-3075, 1991
A;Title: Comparative sequence analysis of the long repeat regions and adjoining parts of A;Reference number: J01494; MUID:92113549; PMID:1662697
A;Accession: J01494
A;Molecule type: DNA
A;Residues: 1-224 <MC5>
A;Csossion: J01494
A;Molecule type: DNA
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C;Genetics:
A;Genetics:
A;Genetic
 transcription regulator, TetR family ameR [imported] - Agrobacterium tumefaciens (strain C.Species: Agrobacterium tumefaciens C.Date: 11-5man-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C.Accession: AD2889
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 Cross-references: GB:AE007869; PIDN:AAK88274.1; PID:g15157738; GSPDB:GN00169
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 h 100.0%; Score 21; DB 2; Length 219; Similarity 100.0%; Pred. No. 1.4e+02; 5; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.4e+02;
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A,Gene: AGR C 4617
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A.Map position: circular chromosome
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Best Local Similarity 100.
Matches 5; Conservative
 Best Local Similarity
Matches 5; Conserva
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Best Local Similarity
Matches 5; Conserv
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 146 SVIAK 150
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146 SVIAK 150
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 1 SVIAK 5
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Gaps

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us-09-890-463-1.rai

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein August 12, 2004, 06:12:47 ; Search time 0.522541 Seconds (without alignments) 493.990 Million cell updates/sec Run on:

US-09-890-463-1 21 1 SVIAK 5 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 seqs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Issued Patents AA:\*
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|          | Description   | -6 Sequence 6, | -14 Sequence 14 | -14 Sequence 1 | 14    | -4236 Sequence 4236 | 196 Sequence | 5388         | Sequence 4, Apr | 36 Sequence 36, | Sequence 4,  | 46           | Sequence      | 6 Sequence 46   | 12172 Sequence | Sequence            | 8 Sequence       | Sequence 88, | 414 Sequence 6414 | 24865           |              | -7825 Sequence | -70 Sequence  | 681A-6760 Sequence 6760, Ap |              | 47,          | 50,          |       |
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| Octavian | ID            | US-09-156-316  | US-08-519-103   | 09-018-        | - 1   | US-09-134-001C      | - 1          | US-09-107-53 | - 1             | US-08-928-94]   | US-09-280-59 | US-09-280-59 | US-09-892-398 | US-09-892-398-4 | US-09-489-03   | US-09-107-532A-5886 | US-08-680-726A-8 | 39-092       | US-09-328-35      | US-09-252-991A- | US-09-381-81 | US-09-328-352  | US-09-465-558 | US-09-543-68                | US-09-323-99 | US-09-323-99 | US-09-323-99 |       |
|          | DB            | 3              | Н               | Ж              | 4     | 4                   | 4            | 4            | m               | ٣               | 4            | 4            | 4             | 4               | 4              | 4                   | Н                | ٣            | 4                 | 4               | m            | 4              | 4             | 4                           | 4            | 4            | 4            |       |
|          | Length        | 50             | 52              | 52             | 52    | 81                  | 102          | 111          | 156             | 156             | 156          | 156          | 156           | 156             | 212            | 244                 | 249              | 249          | 255               | 332             | 342          | 354            | 401           | 436                         | 529          | 529          | 529          | 0 0 0 |
| *        | Query         | 100.0          | 100.0           | 100.0          | 100.0 | 100.0               | 100.0        | 100.0        | 100.0           | 100.0           | 100.0        | 100.0        | 100.0         | 100.0           | 100.0          | 100.0               | 100.0            | 100.0        | 100.0             | 100.0           | 100.0        | 100.0          | 100.0         | 100.0                       | 100.0        | 100.0        | 100.0        |       |
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|          | Result<br>No. | <br>  H<br>  H | 7               | 9              | 4     | Ŋ                   | 9            | 7            | 80              | o,              | 10           | 11           | 12            | 13              | 14             | 15                  | 16               | 17           | 18                | 19              | 20           | 21             | 22            | 23                          | 24           | 25           | 26           |       |

| Sequence 4957, Ap<br>Sequence 11, Appl  | Sequence 11, Appl | Sequence 11, Appl | Sequence 11, Appl | Sequence 11, Appl | Sequence 11, Appl | Sequence 11, Appl | Sequence 7046, Ap  |                   |                  | Sequence 16, Appl | Sequence 24, Appl | Sequence 24, Appl | Seguence 71, Appl | Sequence 71, Appl | Sequence 71, Appl | Sequence 71, Appl |
|-----------------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| US-09-134-000C-4957<br>US-09-335-409-11 | US-09-568-102-11  | US-09-567-969-11  | US-09-568-480-11  | US-09-568-486-11  | US-09-568-472-11  | US-09-567-899-11  | US-09-328-352-7046 | US-08-433-522A-16 | US-09-135-166-16 | US-08-942-046-16  | US-09-107-858-24  | US-09-579-174-24  | US-08-485-455D-71 | US-08-482-130C-71 | US-08-484-211C-71 | US-08-906-769-71  |
| 4 κ                                     | 4                 | 4                 | 4                 | 4                 | 4                 | 4                 | 4                  | m                 | m                | ٣                 | m                 | 4                 | Н                 | ~                 | 7                 | ٣                 |
| 598<br>713                              | 713               | 713               | 713               | 713               | 713               | 713               | 1504               | 32                | 32               | 32                | 48                | 48                | 59                | 59                | 59                | 59                |
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| 8 8 8                                   | 30                | 31                | 32                | 33                | 34                | 35                | 36                 | 37                | 38               | 39                | 40                | 41                | 42                | 43                | 44                | 45                |

### ALIGNMENTS

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APPLICANT: Bernstein, Harold S.
APPLICANT: Bernstein, Harold S.
APPLICANT: Coughlin, Shaun R.
TITLE OF INVENTION: Methods and Compositions for Regulating Cell Cycle
TITLE OF INVENTION: Progression
FILE REFERENCE: UCSF-020/01US
CURRENT APPLICATION NUMBER: US/09/156,316
CURRENT APPLICATION NUMBER: 00/060,688
EARLIER APPLICATION NUMBER: 60/060,688
EARLIER FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 50
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 Sequence 14, Application US/08519103
Patent No. 5733730
GENERAL INFORMATION:
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TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
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US-09-156-316-6; Sequence 6, Application US/09156316; Patent No. 6183961
 ADDRESSEE: KLAUBER & JACKSON
STREET: 411 Hackensack Avenue
CITY: Hackensack
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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US-09-156-316-6
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 US-08-519-103-14
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100.0%; Score 21; DB 3; Length 52; 100.0%; Pred. No. 52;
 Mismatches
 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 APPLICATION NUMBER: 09/018,635
FILING DATE: 04-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DAVIG A. Jackson
 STREET: 411 Hackensack Avenue
 CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
 APPLICANT: de Lange, Titia
Broccoli, Dominique
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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US-09-912-962-14
Sequence 14, Application US/09912962
Patent No. 658657
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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LENGTH: 52 amino acids
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 CITY: Hackensack
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COUNTRY: USA
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 1 SVIAK 5
 1 SVIAK 5
 RESULT 5
US-09-134-001C-4236
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US-09-018-635-14
 US-09-912-962-14
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 Gaps
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 GENERAL INFORMATION:

APPLICANT: de Lange, Titia
APPLICANT: de Lange, Titia
APPLICANT: Broccoli, Dominique
APPLICANT: Smogorzewska, Agata
TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THERBOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
STREET: 411 Hackensack
CITY: Hackensack
CONTRY: USA
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Pred. No. 52;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,103
FILING DATE: 25-AUG-1995
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon B.
REGISTRATION NUMBER: 36,113
REFRENCE/POCKET NUMBER: 600-1-142
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEFAX: 201-343-1684
TELES: 133521
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
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100.0%; Pred. No. ...
0; Mismatches
 600-1-142 CIP1
PC-DOS/MS-DOS
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US-09-018-635-14
Sequence 14; Application US/09018635
Partent No. 6297356
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: David A. Jackson
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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 Smogorzewska, Agata
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FILING DATE: 25-Jul-2001
CLASSIFICATION: <UNKnown>
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 GENERAL INFORMATION:
APPLICANT: Hirai, Hiroshi
APPLICANT: Sherr, Charles
APPLICANT: Sherr, Charles
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
TITLE OF INVENTION: THREOF
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
STREET: Floor
STREET: New Jersey
COUNTRY: USA
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/107,532A
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FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
ATTORNEY/AGENT INFORMATION:
REGIETRATION INFORMATION:
TELEFRANCE/DOCKET NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEFRANCE/TON INFORMATION:
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 NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...111
SEQUENCE DESCRIPTION: SEQ ID NO: 5388:
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 US/08/928,941D
 MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
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SYSTEM: PC-DOS/MS-DOS
 ; Sequence 4, Application US/08928941D; Patent No. 6180763
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TYPE: amino acid
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MEDIUM TYPE: Floppy disk
 COMPUTER READABLE FORM:
 MOLECULE TYPE: protein HYPOTHETICAL: YES
 TOPOLOGY: linear
 Best Local Similarity 100.
Matches 5; Conservative
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OPERATING SYSTEM:
 58 SVIAK 62
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 US-09-107-532A-5388
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 US-08-928-941D-4
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 RESULT 8
 à
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APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERBNCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4236
LENGTH: 81
 APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 .
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 Gaps
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 GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Modamath, Roadoh
APPLICANT: Modamath, Roadoh
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LONG CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475c1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT APPLICATION NUMBER: US/09/370,838
EARLIER APPLICATION NUMBER: US/09/380
SAFINER APPLICATION NUMBER: US/09/285,323
BARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: PASCSEQ for Windows Version 3.0
SEQ ID NO 196
LENGTH: 102
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 100.0%; Score 21; DB 4; Length 81; 100.0%; Pred. No. 82;
 0; Indels
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ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
 Mismatches
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 Sequence 5388, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
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 Sequence 196, Application US/09370838 Patent No. 6444425
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ORGANISM:
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US-09-280-590A-4
 US-09-280-590A-4
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 US-08-928-941D-36

J Sequence 36, Application US/08928941D

J Patent No. 6180763

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APPLICATION NUMBER: US/08/928,941D
 FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
MAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRENGE/DOCKET NUMBER: 1340-1-002 N CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201.487-5800
 ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/POCKET NUMBER: 1340-1-002 N CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
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HYPOTHETICAL: NO
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ORGANISM: Mus musculus
 TELEPAX: 201-343-1684
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HYPOTHETICAL: YES
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CLASSIFICATION:
 79 SVIAK 83
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TOPOLOGY: li
 US-08-928-941D-4
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 CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
 100.0%; Score 21; DB 3; Length 156; 100.0%; Pred. No. 1.6e+02; ative 0; Mismatches 0; Indels
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 Indee, Kazushi
Bodner, Kazushi
Bodner, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
 Indels
 ZIF: 07601

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMITIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,590A
 NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
INFORMATION FOR SEQ ID NO: 4:
 Query Match 100.0%; Score 21; DB 4; L
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Matches 5; Conservative 0; Mismatches 0;
 ORGANISM: Mus musculus
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 FILING DATE: 29-Mar-1999
CLASSIFICATION: <Unknown>
 Sequence 4, Application US/09280590A
Patent No. 6303772
GENERAL INFORMATION:
APPLICANT: Hirai, Hiroshi
 TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
 ATTORNEY/AGENT INFORMATION:
 SEQUENCE CHARACTERISTICS:
 FRAGMENT TYPE: internal ORIGINAL SOURCE:
 CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
Query Match
Best Local Similarity 100..
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 79 SVIAK 83
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 1 SVIAK 5
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
 Length 156;
 Bodner, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
THEREOF
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/109/892,398
FILING DATE: 77-Jun-2001
CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
APPLICATION UNDERS: 09/280,590
FILING DATE: 4UTANDOM:
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON EQ., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-002 N CP2
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 ORGANISM: Mus musculus
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-892-398-4
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TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
 Sequence 46, Application US/09892398 Patent No. 6673902 GENERAL INFORMATION:
 ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 MEDIUM TYPE: Floppy disk
 STRANDEDNESS: «Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
 APPLICANT: Hirai, Hiroshi
Sherr, Charles
Inoue, Kazushi
 NUMBER OF SEQUENCES: 46
 FRAGMENT TYPE: internal ORIGINAL SOURCE:
 ZIP: 07601
COMPUTER READABLE FORM:
 STATE: New Jersey
 STATE: New Jersey
COUNTRY: USA
 TYPE: amino acid
 CITY: Hackensack
 CITY: Hackensack
 Floor
 COUNTRY: USA
 79 SVIAK 83
 1 SVIAK 5
 US-09-892-398-46
 RESULT 13
 ò
 g
 0
 Gaps
 0
 CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
 CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: THE PC Compatible

CORRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/280,590A

FILING DATE: 29-Mar-1999

CLASSIFICATION: «Unknown»

ATTORNEY/AGENT INPORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REGISTRATION NUMBER: 1340-1-002 N CP2

TELECOMMUNICATION NUMBER: 1340-1-002 N CP2

TELECOMMUNICATION NUMBER: 1340-1-002 N CP2

TELEPHONE: 201-487-5800

TELEPAX: 201-343-1644

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:
 Length 156;
 TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES THEREOF
 Bodner, Sarah M.
TITLE OF INVENTION: CYCLIN-D BINDING FACTOR, AND USES
THEREOF
 0; Indels
 100.0%; Score 21; DB 4; 100.0%; Pred. No. 1.6e+02; iive 0; Mismatches 0;
 ; ORGANISM: Gallus gallus ; SEQUENCE DESCRIPTION: SEQ ID NO: 46: US-09-280-590A-46
 Sequence 46, Application US/09280590A
Patent No. 6303772
GENERAL INFORMATION:
APPLICANT: Hiral, Hiroshi
Sherr, Charles
 Sequence 4, Application US/09892398 Patent No. 6673902 GENERAL INFORMATION:
 TYPE: amino acid
STRANDENDESS: «Unknown»
TOPOLLGY: linear
MOLECULE TYPE: protein
 LENGTH: 156 amino acids
 Sherr, Charles
Inoue, Kazushi
Bodner, Sarah M.
 Sherr, Charles
Inoue, Kazushi
 APPLICANT: Hirai, Hiroshi
 HYPOTHETICAL: YES
FRAGMENT TYPE: «Unknown»
ORIGINAL SOURCE:
 ZIP: 07601
COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 46
 STATE: New Jersey
COUNTRY: USA
 Query Match
Best Local Similarity 100.
Matches 5; Conservative
 CITY: Hackensack
 NUMBER OF SEQUENCES:
 Floor
 79 SVIAK 83
 1 SVIAK 5
US-09-280-590A-46
 US-09-892-398-4
 RESULT 12
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Gaps

0;

Indels

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 Faceton No. 6610836
GENERAL INFORMATION:
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT PILING DATE: 000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 212
 RESULT 15
US-09-107-532A-5886
; Sequence 5886, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TILLE OF INVENTION: BUTEROCCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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 Query Match
100.0%; Score 21; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
 Length 212;
 0; Indels
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 26,742
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-497-5800
 TELEPHONE: 201-497-1684
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 SEQUENCE CHARACTERISTICS:
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 STRANDEDNESS: «Unknown»
TOPOLLGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
FRAGWENT TYPE: «Unknown»
ORIGINAL SOURCE:
CRGANISM: Gallus Gallus
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APPLICATION NUMBER: US/09/892,398
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/280,590
 FILING DATE: 27-Jun-2001
CLASSIFICATION: <Unknown>
 LENGTH: 156 amino acids TYPE: amino acid
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0
 TYPE: PRT
ORGANISM: Klebsiella pneumoniae
 Conservative
 Query Match
Best Local Similarity
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 36 SVIAK 40
 1 SVIAK 5
 1 SVIAK 5
 US-09-489-039A-12172
 US-09-489-039A-12172
 US-09-892-398-46
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 1714 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPAX: (781)893-5007
TELEPAX: (781)893-5007
TELEPAX: (781)893-5007
TELEPAX: (781)893-5007
TELEPAX: (781)893-5007
 NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...244

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 ORGANISM: Enterococcus faecium
 Search completed: August 12, 2004, 06:21:04 Job time : 1.52254 secs
 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
 100 Beaver Street
 LENGTH: 244 amino acids TYPE: amino acid
 STATE: Massachusetts
COUNTRY: USA
 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
 Ouery Match
Best Local Similarity 100.
 CITY: Waltham
 ORIGINAL SOURCE:
 186 SVIAK 190
 1 SVIAK 5
 FEATURE
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
 Copyright
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- nucleic search, using sw model OM nucleic

August 13, 2004, 11:19:50 ; Search time 77 Seconds (without alignments) 6061.217 Million cell updates/sec Run on:

US-09-890-463-6 841 Title: Perfect score:

1 toogttatogotaaacagat.......aaaagoggoogotogaatta 841 IDENTITY NUC Scoring table: Sequence:

682709 seqs, 277475446 residues Searched:

Gapop 10.0 , Gapext 1.0

1365418 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA: \* Database

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3: /cgm2 6/ptcdata/2/ina/6A COMB.seq:\*
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5: /cgm2 6/ptcdata/2/ina/PcTUS COMB.seq:\*
6: /cgm2 6/ptcdata/2/ina/PcTUS COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |                       |             | Appli           | App1i           | Appli           | Appli           | Appli           | Appli           | Appli           | App1              | Appl              | Appl              | Appl              | Appl             | Appli           | Appl             | Appl              | Appl             | Appl              | App,              |                   | г.,              | Appl             | Appli           | App.              | Appl             | Appl             | Appl             | Appl             |
|-----------|-----------------------|-------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-------------------|-------------------|-------------------|-------------------|------------------|-----------------|------------------|-------------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|-----------------|-------------------|------------------|------------------|------------------|------------------|
|           | Ę                     | 1           | 9               | 'n              | 7               | ر<br>ای         | س               | 4.              |                 | 15,               | 64,               | 64,               | 64,               | 15,              | ,<br>,          | 30,              | 30,               | 31,              | 31,               | 216               | 362               | 53,              | 53,              | H               | 151               | 14,              | 26,              | 78,              | 99               |
|           | Description           | DESCT TRUTT | Sequence          | Sequence          | Sequence          | Sequence          | Sequence         | Sequence        | Sequence         | Sequence          | Sequence         | Sequence          | Sequence          | Sequence          | Sequence         | Sequence         | Sequence        | Sequence          | Sequence         | Sequence         | Sequence         | Sequence         |
| SUMMARIES | I.D                   | T.          | US-09-459-956-6 | US-09-459-956-5 | US-09-459-956-7 | US-09-459-956-2 | US-09-459-956-3 | US-09-459-956-4 | US-09-839-650-1 | US-09-609-161B-15 | US-09-626-581D-64 | US-09-415-765B-64 | US-09-626-580C-64 | US-09-277-716-15 | US-09-839-650-2 | US-09-277-716-30 | US-09-609-161B-30 | US-09-277-716-31 | US-09-609-161B-31 | US-09-385-982-216 | US-09-385-982-362 | US-09-640-173-53 | US-09-713-550-53 | US-09-769-987-1 | US-09-370-838-151 | US-08-232-463-14 | US-08-702-344-26 | US-09-800-729-78 | US-09-336-536-66 |
|           | DR.                   | 3           | 4               | 4               | 4               | 4               | 4               | 4               | 4               | 4                 | 4                 | 4                 | 4                 | ď                | 4               | m                | 4                 | 'n               | 4                 | 3                 | m                 | 4                | 4                | 4               | 4                 | ٦                | П                | 4                | 4                |
|           | Query<br>Match Length |             | 678             | 669             | 801             | 069             | 969             | 969             | 720             | 1079              | 1079              | 1079              | 1079              | 1085             | 1021            | 1104             | 1104              | 1279             | 1279              | 322               | 322               | 396              | 396              | 6412            | 3275              | 7218             | 144              | 1141             | 1927             |
| æ         | Query                 | 110000      | 45.6            | 43.1            | 32.6            | 23.6            |                 | 18.0            | 15.6            | 15.0              | 15.0              | 15.0              | 15.0              | 15.0             |                 |                  | 14.6              | 14.2             |                   | 0.9               | ٠                 | 5.9              | 5.9              |                 | 5.7               | ٠                | 5.5              | 5.5              | 5.5              |
|           | Score                 | 1 (         | ω               | 362.6           | 274             | 198.4           | 154.2           |                 | 131.6           | 126               | 126               | 126               | 126               | 126              | 122.8           | 122.6            | 122.6             | 119.4            | 119.4             | 50.4              | 50.4              | 49.6             | 49.6             | 48.4            | 47.8              | 46.8             | 46.2.            | 46               | 46               |
|           | Result<br>No.         |             | ת               | 7               | e               | 4               | Ŋ               | 9               | 7               | 80                | σ                 | 10                | 11                | 12               | 13              | 14               | 15                | 16               | 17                | c 18              | c 19              | c 50             |                  | 22              | 23                | c 24             | 25               | 26               | 27               |

| Sequence 33, Appl | Sequence 10, Appl | Sequence 10, Appl | 4, A            | Sequence 3, Appli | m               | М               | Sequence 3, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 1, Appli | Sequence 9596, Ap  | Sequence 465, App  | Sequence 465, App  | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| US-09-800-729-33  | US-09-640-173-10  | US-09-713-550-10  | US-08-202-056-4 | US-08-076-093A-3  | US-08-701-265-3 | US-08-284-586-3 | US-08-805-478-3   | US-08-802-627A-3  | US-08-801-238-3   | US-08-801-228-3   | US-09-104-296-3   | PCT-US94-06380-2  | US-08-379-482A-2  | US-09-967-908A-1  | US-09-621-976-9596 | US-09-620-405B-465 | US-09-433-826B-465 |
| 4                 | 4                 | 4                 | Н               | Н                 | Н               | 7               | 7                 | 7                 | N                 | ~                 | m                 | S                 | 7                 | 4                 | 4                  | 4                  | 4                  |
| 2394              | 396               | 396               | 1737            | 1737              | 1737            | 1737            | 1737              | 1737              | 1737              | 1737              | 1737              | 1737              | 1738              | 6409              | 194                | 674                | 674                |
| 5.4               | 5.4               | 5.4               | 5.4             | 5.4               | 5.4             | 5.4             | 5.4               | 5.4               | 5.4               | 5.4               | 5.4               | 5.4               | 5.4               | 5.4               | 5.4                | 5.3                | 5.3                |
| 45.8              | 45.6              | 45.6              | 45.6            | 45.6              | 45.6            | 45.6            | 45.6              | 45.6              | 45.6              | 45.6              | 45.6              | 45.6              | 45.6              | 45.4              | 45.2               | 44.8               | 44.8               |
| 28                | ۵ 29              | c 30              | 31              | 32                | 33              | 34              | 35                | 36                | 37                | 38                | 39                | 40                | 41                | 42                | 43                 | 44                 | 45                 |

#### ALIGNMENTS

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 64 TITGAGGICGAAGGCGAIGGAAAAGGAAAGCCTTACGAGGGGGGAGCAGACGGTAAGGCTG 123
 79 TITGAAATAGAAGGCGAAGGAGGGGGCCATACGAAGGCCACAATACCGTAAAGCTT 138
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 244 TICCCGGGGAGATATACATGGGAGGATCATGAACTITGAAGATGGTGCAGTGTACT 303
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 Gaps
 APPLICANT: Taien, Noger Y.
APPLICANT: Gonzalez, III, Jesus E.
APPLICANT: Gonzalez, III, Jesus E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
FILE REFERENCE: REGEN1290-4
CURRENT FELLING DATE: 1999-05-08
PRIOR FILING DATE: 1999-05-08
PRIOR FILING DATE: 1999-05-08
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTERQ for Windows Version 4.0
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 Score 383.6; DB 4; Length 678;
Pred. No. 1.4e-92;
0; Mismatches 169; Indels 0;
 Sequence 6, Application US/09459956
Patent No. 6342379
 Query Match
Best Local Similarity 74.2%;
Matches 485; Conservative
 ; ORGANISM: Discosoma sp
US-09-459-956-6
 GENERAL INFORMATION:
 678
US-09-459-956-6
 259
 TYPE: DNA
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438
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259 TTTCCGGAGGGATATACATGGGAACGGTCCATGCACTTTGAAGACGGTGGCTTGTGTGTTGT 318
 423
 ACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAG 483
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 TRANSMEMBRANE POTENTIALS BY
 Length 801,
 32.6%; Score 274; DB 4; Length 80 64.2%; Pred. No. 1.9e-63; ive 0; Mismatches 230; Indels
 APPLICANT: TSien, Roger Y.
APPLICANT: TSien, Roger Y.
APPLICANT: Genzalez, III Josus E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBR.
TITLE OF INVENTION: OFTICAL METHODS
FILE REFERENCE: REGENI290-4
CURRENT FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 08/76,860
PRIOR PELING DATE: 1999-05-08
PRIOR PELING DATE: 1999-05-08
PRIOR PELING DATE: 1995-06-07
PRIOR PELING DATE: 1996-06-07
PRIOR PLILING DATE: 1996-06-07
 NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
 ; Sequence 7, Application US/09459956
; Patent No. 6342379
 Matches 412; Conservative
 ; TYPE: DNA
; ORGANISM: Clavularia sp
US-09-459-956-7
 Query Match
Best Local Similarity
 LENGTH: 801
 544
 601
 75
 135
 195
 324
 304
 364
 424
 SEQ ID NO 7
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 303
 498
 558
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 618
 TTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTG 123
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 APPLICANT: TROUGHLIAN:
APPLICANT: Gonzalez, III, Jesus E.
APPLICANT: Gonzalez, III, Jesus E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
TITLE OF INVENTION: OPTICAL METHODS
FILE REFERENCE: REGENI290-4
CURRENY APPLICATION NUMBER: US/09/459,956
CURRENY FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR APPLICATION NUMBER: 08/481,977
PRIOR APPLICATION NUMBER: PS5-06-07
PRIOR PILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR PILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
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 Indels
 Score 362.6; DB 4;
Pred. No. 5.3e-87;
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US-09-459-956-5
Sequence 5, Application US/09459956
Patent No. 6342379
GENERAL INFORMATION:
 Query Match 43.1%;
Best Local Similarity 73.1%;
Matches 480; Conservative
 TYPE: DNA ORGANISM: Discosoma striata
 LENGTH: 699
 US-09-459-956-5
 439
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 SEQ ID NO 5
 379
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 504
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 479 IGAAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTACAAGGCAAAGA
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 Gaps
 12;
 Sequence 3, Application US/0945956

Patent No. 6342379

GENERAL INFORMATION:

APPLICANT: Genzalez, III, Jesus E.

APPLICANT: Genzalez, III, Jesus E.

TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY CURRENT APPLICATION NUMBER: US/09/459,956

CURRENT FILING DATE: 1999-12-13

PRIOR FILING DATE: 1999-05-08

PRIOR FILING DATE: 1999-06-07

PRIOR FILING DATE: 1996-06-07

PRIOR FILING DATE: 1996-06-07

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FRASEC for Mindows Version 4.0
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 18.3%; Score 154.2; DB 4; Length 58.0%; Pred. No. 1.2e-31; tive 0; Mismatches 218; Indels
 Matches 317; Conservative
 ; ORGANISM: Zoanthus sp
US-09-459-956-3
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Best Local Similarity
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 179 GTCAGTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCTGACTATGTAAAGC 238
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 125 CTGTCA-----CCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGT 178
 TCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCT 434
 AGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTC 614
 684 AGACTATCACTTTGTGGACCATTGGATTCTTGAACCATGACAAGGATTACAACAA 743
 80 TTACCGICAAAGGIGAAGGCAACGGGAAGCCATACGAAGGGACGCAGACTICGACTITIA 139
 140 AAGTCACCATGGCCAACGGTGGGCCCCTTGCATTCTCCTTTGACATACTATCTACAGTGT 199
 20 TIAICGGAGAIGACAIGAAAAIGACCIACCAIAIGGAIGGCIGIGICAAIGGGCAIIACI 79
 504 TCCCAATGGTCCGGTTATGCAGAAAAAACTTTGAAGTGGGAACCATCCACTGAGATTAT
384 ATATTCCTGGGAAAGAACCATGACTTTTGAAGACAAAGGCATTGTCAAAGTGAAAGTGA
 444 CATAAGCATGCAGGAAGACTCCTTTATCTATGAAATTCGTTTTGATGGGATGAACTTTCC
 CITTGCACGAGATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAGG
 TGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAAGATGCC
 TGGCCATTACCGATGTGACTTCAAAGTATTTACAAAGGAAAAAAGTTGTCAAATTGCC
 315 TICCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCC
 TTATCGCTAAACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACACTACT
 Gaps
 9
 Score 198.4; DB 4; Length 690;
Pred. No. 2.1e-43;
0; Mismatches 276; Indels 6
 APPLICANT: GONZALEZ, III, Jesus E.
APPLICANT: GONZALEZ, III, Jesus E.
TITLE OF INVENTION: DFIECTION OF TRANSMEMBRANE POTENTIALS BY
TITLE OF INVENTION: OPTICAL METHODS.
FILE REFERENCE: REGEN1290-4
CURRENT PILING DATE: 1999-12-13
PRIOR PILING DATE: 1999-05-08
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR PILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
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 744 AGTAACGCTGTATGAGAATGCAGTTGCTCGCTATTCTTTGCT 785
 Sequence 2, Application US/09459956
Patent No. 6342379
GENERAL INFORMATION:
 23.6%;
 Query Match 23.6
Best Local Similarity 57.4
Matches 380; Conservative
 ; TYPE: DNA
; ORGANISM: Anemonia majano
US-09-459-956-2
 SEQ ID NO 2
LENGTH: 690
 435 (
 375
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GENERAL INFORMATION:
APPLICANT: Stratagene
TITLE OF INVENTION: Humanized Polynucleotide Sequence Encoding Renilla Mulleri Green
Patent No. 6645761
TITLE OF INVENTION: Fluorescent Protein
FILE REFERENCE: 25436/1755
CURRENT APPLICATION NUMBER: US/09/839,650
CURRENT FILING DATE: 2001-04-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
149 AAGGGGGACCATTGCCATTTTCCGAAGACATATTGTCAGCTGGCTTTAAGTACGGAGACA 208
 209 ggartricacrgaararccrcaagacaragragacrarricaagaacrcgrgrgrgcrg 268
 269 gararacanggecanggrerrirererringangganggangrerigearangcaargrag 328
 329 ATATAACAGTGAGTGTCAAAGGAAACTGCATTTATCATAAGAGCATATTTAATGGAATGA 388
 368 ACTITCCICCCAATGGACCTGTIAIGCAGAAGAAGAACACAGGGCTGGGAACCCAACACTG 427
 AGCGTCTTTTGCACGA-----GATGGAATGCTGATAGGAAACAACTTTATGGCTCTGA 481
 AGAAGATCATGCCAGTACCTAAGCAGGGGATACTGAAAGGGGATGTCTCCATGTACTCC 508
 482 AGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAG---A 538
 509 TICTGAAGGATGGTGGGCGTTACCGGTGCCAGTTCGACACAGTTTACAAAGCAAAGTCTG 568
 GATGAGCTACAAGCTGAACCTGGAGGCATCGTGAACAACCACGTGTTCACCATGGAGGG 104
 105 CTGCGGCAAGGGCAACATCCTGTTCGGCAACCAGCTGGTGCAGATCCGCGTGAAGGG 164
 CGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCATACC 197
 ceccecerecerrecerredacarcarcardacececerrecacracacaracecae 224
 ATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGGGGAGATA 257
 GATATACATGGGAGAGCATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATG
 CGATGGAAAAGGAAAAGCCTTACGAGGGGGAGCAGACGCTAAAGGCTGTCACCAAGGG
 GATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAAGG
 TACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGGGA
 AT-----TCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGA
 0
 Score 131.6; DB 4; Length 720;
Pred. No. 1.2e-25;
0; Mismatches 309; Indels 0.
 539 AGCCTGTGAAGATGCCAGGGTATCACTATGTTGACCGCAAACT 581
 569 recenagradarecegaereceacircarecagearanger 611
 OTHER INFORMATION: Humanized R. mulleri polynucleotide NAME/KEY: misc feature LOCATION: (1) - (720) OTHER INFORMATION: Humanized DNA sequence
 Sequence 1, Application US/09839650 ; Patent No. 6645761
 0,
 15.6%;
50.6%;
 TYPE: DNA ORGANISM: Artificial Sequence
 Query Match 15.6
Best Local Similarity 50.6
Matches 317; Conservative
 SEQ ID NO 1
LENGTH: 720
 US-09-839-650-1
 ; OTHER INFUR
US-09-839-650-1
 389
 194
 428
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 FEATURE:
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 AGGCCGCACCTCTGCCATTTGCTTGCGATATTTTATCACCACAGTGTCAGTACGGAAGCA 193
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 438 GCCATCCTGCGAGAAGATCATACCAGTACCTAAGCAGGGGATATTGAAAGGGGATGTCTC 497
 73
 88
 GGCTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGATATTTTATCACCACAGTGTCA
 183 GTACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTC
 243 ATTCCCGGGGAGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAG----T
 GIGTCCTGCTGGATATACATGGGACAGGTCTTTTCTCTTTGAGGATGGAGCAGTTTGCAT
 GTGTACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTT
 318 Argraniccagararancagrengagrerrgagaaaaacrecargrarcargagrecaaarr
 357 CTCTGGTTTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGA
 11 ACCCAACACTGAGCGTCTCTTTGCACGA-----GATGGAATGCTGATAGGAAACAACTT
 TATGGCTCTGAAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTAAA
 498 cangracchcchrchgaagganggregecgrinnacegreccaahhicaacacharhacaa
 14 AACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACACTATTGAGGTCG
 aagaaatgacaatgaataccacatggaagggtgcgtcaacggacataaatttgtgatca
 Gaps
 15;
 Length 696;
 GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Gonzalez, III, Jesus E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
TITLE OF INVENTION: OPTICAL METHODS
 Indels
 Score 151.8; DB 4;
Pred. No. 5e-31;
0; Mismatches 232;
 CURRENT APPLICATION NUMBER: US/09/459,956
CURRENT APPLICATION NUMBER: US/09/459,956
CURRENT FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR PRILING DATE: 1999-05-08
PRIOR PRILING DATE: 1995-06-07
PRIOR PRILING DATE: 1995-06-07
PRIOR PRILING DATE: 1996-06-06
NUMBER: PCT/US96/09652
PRIOR FILING DATE: 1996-06-06
NUMBER: PCT/US96/09652
SEQ ID NOS: 22
SEQ ID NOS: 22
 Sequence 4, Application US/09459956
Patent No. 6342379
 18.0%;
57.6%;
 Query Match
Best Local Similarity 57.67
Matches 336; Conservative
 531 GGCAAAG 537
 TYPE: DNA ORGANISM: ZOANThus sp
 558 AĞCAAAĞ 564
 LENGTH: 696
 ; UKGANISM: 24
US-09-459-956-4
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416 AAGGGCCCCACTGCCTTTTGCATTTGATATTGTCTCACCAGCTTTTCAATATGGCAACC 475
 356 AGGGTTGCGGCAAAGGGAATATTTTATTCGGCAATCAACTGGTTCAGATTCGTGTCACGA 415
 194 TACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGGGA 253
 374 CTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCCAACACTGAGCGTC 433
 656 CAGATGATGGTCCCGTCATGCAGAAGACTATCTTAGGAATAGAGCCTTCATTTGAAGCCA 715
 836 TICCTICGTAICATTTTAITCAACATCGTTTGGAAAAGACTTACGTAGAAGACGGGGGGT 895
 GENERAL INFORMATION:

APPLICANT Anderson, David

TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide

TITLE OF INVENTION: Libraries

TITLE OF INVENTION: Libraries

TITLE OF INVENTION: Libraries

FILE REFERENCE: A-66900-3/RMS

CURRENT FILING DATE: 2000-07-27

PRIOR PILING DATE: 1999-10-08

PRIOR FILING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PATENTION NUMBER: 07415,765

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PATENTION NUMBER: 07415,765

SOFTWARE: PATENTION NUMBER: 07415,765

SOFTWARE: PATENTION NUMBER: 07415,765
 476 GTACTTTCACGAAATATCCGAATGATATATCAGATTATTATACAATCATTTCCAGCAG
 776 GGAAATATTATTCATGTCACATGAAAACATTAATGAAGTCGAAAGGTGTAGTAAAGGAGT
 ATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGGTTTGAACTTTC
 ATATAAATTTAATAGAAGACAAGTTCGTCTACAGAGTGGAATACAAAGGTAGTAACTTCC
 TCTTTGCACGAGATGCAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAG
 TGTACATGAATAATGGCGTCTTGGTCGGCGAAGTAATTCTTGTCTATAAACTTAAACTCTG
 GTGGTCACTATTTGTGTGAATTCAAATCTACAAGGCAAAGAAGCCTGTGAAGATGC
 554 CAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGATTACACTT
 Gaps
 0
 Indels
 Query Match 15.0%; Score 126; DB 4; Lv
Best Local Similarity 50.0%; Pred. No. 4.2e-24;
Matches 315; Conservative 0; Mismatches 315;
 896 redrichachdeardacherachtreche 925
 614 CCGTTGAGCAGTGTGAAATTTCCATTGCAC 643
 US-09-626-581D-64; Sequence 64, Application US/09626581D; Patent No. 6548249
 TYPE: DNA
ORGANISM: Renilla muelleri
 ; LOCATION: (259)..(975)
; OTHER INFORMATION:
US-09-626-581D-64
 FEATURE:
NAME/KEY: CDS
LOCATION: (259
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 GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
APPLICANT: Bryan, Bruce
APPLICANT: Bryan, Bruce
APPLICANT: Bryan, Bruce
APPLICANT: Brown, Ucireracies, Ind.
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIPERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIC
TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIC
TITLE OF INVENTION: AND FLUORESCENT PROTEINS
TILLE OF INVENTION: AND FLUORESCENT PROTEINS
FILLE REPRENCE: 24729-121B
CURRENT APPLICATION NUMBER: US/09/609,161B
CURRENT FILLING DATE: 1998-03-26
PRIOR FILLING DATE: 1998-06-15
PRIOR PELLING DATE: 1998-06-15
PRIOR APPLICATION NUMBER: 60/099,367
PRIOR APPLICATION NUMBER: 60/099,367
PRIOR FILLING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VOIL SECOND OF SEQ ID NOS: 32
LENGTH: 1079
 HIG
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437
 405 caacasccccarangcadaadaccarccrasscarcaasccaacarara 464
 438 IGCACGAGAIGGAAIGCIGAIAGGAAACAACTITIAIGGCICTGAAGIIAGAAGGAGGIGG 497
 524
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 296 AAGTAATGTCGTATAAAGTAAATCTGGAAGGAATTGTAAACAACCATGTTTTTACAATGG 355
 TACATGGGAGGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGATTC 317
 CAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTCCTCC 377
 345 chaccigarceaggachagirceigirácegeregaerhehaggegaggaacirceega 404
 73
 CATGAACAACGCGTGCTGGTGGCGAGGTGATCCTGGTGTACAAGCTGAACAGCGGCAA
 GTACTACAGCTGCCACATGAAGACCCTGATGAAGAGCAAGGGCGTGGTGAAGGAGTTCCC
 285 cárgiacsáccicociócsciracsássácsácsissorsásasaricoscassar
 378 CAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCCAACACTGAGCGTCTCTT
 GTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTTCCGT
 TCACTATTTGTGTGAATTCAAATCTACTAAGAGGCAAAGAAGCCTGTGAAGATGCCAGG
 14 AACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCG
 Gaps
 ; LOCATION: (259)..(975)
; OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP)
US-09-609-161B-15
 Length 1079;
 Score 126; DB 4; Length 10
Pred. No. 4.2e-24;
0; Mismatches 315; Indels
 TGAGCAGTGTGAAATTTCCATTGCAC 643
 645 GGAGCACGAGACCGCCATCGCCC 670
 Sequence 15, Application US/09609161B
Patent No. 6436682
 Query Match
Best Local Similarity 50.0%;
Matches 315; Conservative
 TYPE: DNA
ORGANISM: Renilla mulleri
 US-09-609-161B-15
 NAME/KEY: CDS
 465
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ORGANISM: Renilla muelleri
 ; LOCATION: (259)..(975);
; OTHER INFORMATION:
US-09-626-580C-64
 NAME/KEY: CDS
 SEQ ID NO 64
LENGTH: 10
 596
 74
 356
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 TYPE: DNA
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 CTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTC 433
 194 TACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGGGA 253
73
 | Sequence 64, Application US/09415765B | Satent No. 6548632 | Satent No. 6548632 | GENERAL INFORMATION: | APPLICANT: Anderson, David | TITLE OF INVENTION: Libraries | CURRENT APPLICATION NUMBER: US/09/415,765B | CURRENT FILING DATE: 1999-10-08 | PRIOR PILING DATE: 1999-10-08 | PRIOR PILING DATE: 1999-10-08 | NUMBER OF SEQ ID NOS: 65 | SOFTWARE PARENTIN VET. 2.0 | SOFTWARE PARENTIN
 656 CAGATGATGGTCCCGTCATGCAGAAGACTATCTTAGGAATAGAGCCTTCATTTGAAGGCCA
 134 AGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCA
AACAGATGACCTACAAAGTTTATATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCG
 296 AAGTAATGTCGTATAAAGTAAATCTGGAAGGAATTGTAAACAACCATGTTTTTACAATGG
 356 AGGGTTGCGGCAAAGGGAATATTTTATTCGGCAATCAACTGGTTCAGATTCGTGTCACGA
 AAGGGGCCCCACTGCCTTTTGCATTTGATATTGTGTCACCAGCTTTTCAATATGGCAACC
 GTACTTTCACGAATTATCCAATGATATCAGATTATTTTTATACAATCATTTCCAGCAG
 GATATACATGGGAGGATCATGAACTTTGAAGATGGTGCAGTGTACTGTCAGCAATG
 GATTTATGTATGAACGAACATTACGTTACGAAGATGGCGGACTTGTTGAAATTCGTTCAG
 ATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTC
 ATATAAATTTAATAGAAGACAAGTTCGTCTACAGAGTGGAATACAAAGGTAGTAACTTCC
 TCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAG
 TGTACATGAATAATGGCGTCTTGGTCGGCGAAGTAATTCTTGTCTATAAACTTAAACTCTG
 GTGGTCACTATTTGTGTGAATTCAAATCTTACAAGGCAAAGAAGCCTGTGAAGATGC
 GGAAATATTATTCATGTCACATGAAACATTAATGAAGTCGAAAGGTGTAGTAAAGGAGT
 554 CAGGGTATCACTATGTTGACCGCAAACTGGGATGTAACCAATCACAAGGATTACACTT
 836 TTCCTTCGTATCATTTTATTCAACATCGTTTGGAAAAGACTTACGTAGAAGACGGGGGGT
 Gaps
 0;
 15.0%; Score 126; DB 4; Length 1079; ilarity 50.0%; Pred. No. 4.2e-24; Conservative 0; Mismatches 315; Indels
 614 CCGTTGAGCAGTGTGAAATTTCCATTGCAC 643
 896 redricaacacardacacrecrarrecre 925
 TYPE: DNA ORGANISM: Renilla muelleri
 ; LOCATION: (259)..(975)
; CTHER INFORMATION:
US-09-415-765B-64
 Query Match
Best Local Similarity
Matches 315; Conserv
 FEATURE:
NAME/KEY: CDS
LOCATION: (259)
 RESULT 10
US-09-415-765B-64
 LENGTH: 1079
 416
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 AGGITGCGGCAAAGGGAATATTTTATTCGGCAATCAACTGGTTCAGATTCGTGTCACGA 415
 134 AGGGCGGACCICTGCCATTIGCTTGGGAIATTTTAICACCACAGIGTCAGIACGGAAGCA 193
 AAGGGCCCCACTGCCTTTTGCATTTGATATTGTCCACCAGCTTTTCAATATGGCAACC 475
 TACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGGGA 253
 GATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATG 313
 GATTTATGIATGAACGAACATTACGTTACGAAGATGGCGGACTTGTTGAAATTCGTTCAG 595
 ATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGTTTGAACTTTC 373
 CTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTC 433
 cagargargerecegreargeagaagaerarerraggaaragageerrearrigaageea 715
 493
 TGTACATGAATAATGGCGTCTTGGTCGGCGAAGTAATTCTTGTCTATAAACTAAACTCTG 775
 553
 GGAAATATTATTCATGTCACATGAAACATTAATGAAGTCGAAAGGTGTAGTAAAGGAGT 835
 CAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAACAAGGATTACACTT 613
 Trectregrateatriatreaacatestregaaaaacertegaaaageregaegageser 895
73
 GTGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAAGATGC
 AAGTAATGTCGTATAAAGTAAATCTGGAAGGAATTGTAAACAACCATGTTTTTACAATGG
 ATATAAATTTAATAGAAGACAAGTTCGTCTACAGAGTGGAATACAAAGGTAGTAACTTCC
AACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCG
 TCTTTGCACGAGATGCAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTAGAAGGAG
 CCGTTGAGCAGTGTGAAATTTCCATTGCAC 643
 rcerridaacadcardaacacrecrarrecre 925
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RESULT 11

RESULT 11

US-09-626-580C-64

US-09-626-580C-64

Sequence 64, Application US/09626580C

Patent No. 6562617

GENERAL INPORMATION:

APPLICANT: Anderson, David

APPLICANT: Bogenberger, Jakob M.

APPLICANT: Beele, Beau R.

TITLE OF INVENTION: FUSIONS OF SCAFFOLD PROTEINS WITH RANDOM PEPTIDE LIBRARIES

FILE REFERENCE: A-66900-2/RMS/AMS

CURRENT APPLICATION NUMBER: US/09/626,580C

CURRENT FILING DATE: 1999-10-08

PRIOR FILING DATE: 1999-10-08

PRIOR FILING DATE: 1998-10-08

PRIOR FILING DATE: 1998-10-08

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIN Version 3.1

SEQ ID NO 64

LENGTH: 1079

TYPE: DA

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614 CCGTTGAGCAGTGTGAAATTTCCATTGCAC 643
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FEATURE:
NAME/KEY: CDS
LOCATION: (259)..(975)
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TYPE: DNA
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LID.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
CURRENT APPLICATION NUMBER: US/09/277,716A
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/102,939
EARLIER APPLICATION NUMBER: 60/089,367
EARLIER FILING DATE: 1998-06-15
EARLIER APPLICATION NUMBER: 60/099,624
EARLIER APPLICATION NUMBER: 60/079,624
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                         AAGTAATGTCGTATAAAGTAAATCTGGAAGGAATTGTAAACAACCATGTTTTTACAATGG 355
                                                                                                                                                           AGGGTTGCGGCAAAGGGAATATTTTATTCGGCAATCAACTGGTTCAGATTCGTGTCACGA 415
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               Length 1079;
               Score 126; DB 4; Length 10 Pred. No. 4.2e-24; 0; Mismatches 315; Indels
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               15.0%;
               Query Match
Best Local Similarity 50.03
Matches 315; Conservative
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TYPE: DNA
ORGANISM: Renilla mulleri
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RESULT 13
US-09-839-650-2
US-09-839-650-2
Sequence 2, Application US/09839650
Patent No. 6645761
GENERAL INFORMATION:
APPLICANT: Stratagene
TILLS OF INVENTION:
Patent No. 6645761
TILLE OF INVENTION: Fluorescent Protein
PILE REPERENCE: 26436/1755
CURRENT APPLICATION NUMBER: US/09/839,650
CURRENT APPLICATION NUMBER: US/09/839,650
CURRENT FILING DATE: 2001-04-19
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
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; OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein US-09-277-716-15
                                                                                                             Length 1085
                                                                                                  Query Match 15.0%; Score 126; DB 3; Length 10 Best Local Similarity 50.0%; Pred. No. 4.2e-24; Matches 315; Conservative 0; Mismatches 315; Indels
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Best Local Similarity 49.8%;
Matches 311; Conservative
2.0
                                       TYPE: DNA
ORGANISM: Ptilosarcus gn
FEATURE:
NAME/KEY: CDS
SOFTWARE: Patentin Ver.
SEQ ID NO 30
LENGTH: 1104
                                                                                                   LOCATION: (34)..(747)
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US-09-609-161B-30
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
CURRENT APPLICATION NUMBER: US/09/277,716A
EARLIER PILING DATE: 1998-10-01
EARLIER PLING DATE: 1998-10-01
EARLIER PLING DATE: 1998-06-15
EARLIER PLING DATE: 1998-06-15
EARLIER PILING DATE: 1998-06-15
EARLIER PILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
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                                                                                     Length 1021;
                                                                                                                 0; Mismatches 317; Indels
                                                                                     DB 4;
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Pred. No. 2.9e-23
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                                                                                    14.6%;
                                                                                                  Best Local Similarity 49.7
Matches 313; Conservative
ORGANISM: Renilla muelleri
                        NAME/KEY: exon
LOCATION: (259)..(976)
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GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
APPLICANT: Bryan, Bruce
APPLICANT: Bryan, Bruce
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-121B
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      (insert
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                                                                                                                                                         Gaps
                                                                                                                                                         ..
      (GFP)
                                                                                            Length 1104;
                                                                                                                                                         Indels
; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein US-09-277-716-30
                                                                                         Score 122.6; DB 3;
Pred. No. 3.4e-23;
); Mismatches 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          643
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                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: CDS
I LOCATION: (34)..(747)
COTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (insert A)
US-09-609-161B-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 ATGAACAGGGGGTTCTGGTGGGGGAAGTAGATCTCGTTTACAAACTCGAGTCAGGGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 49.8%; Pred. No. 3.4e-23;
Matches 311; Conservative 0; Mismatches 314; Indels 0;
CURRENT APPLICATION NUMBER: US/09/609,161B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             676 GAACACACGAGACGCCATTGCAC 700
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                CURRENT FILING DATE: 2000-06-30
FRICAR PAPLICATION NUMBER: 09/2777,716
FRICAR PAPLICATION NUMBER: 09/2777,716
FRICAR FILING DATE: 1999-03-26
FRICAR FILING DATE: 1998-10-01
FRICAR FILING DATE: 1998-10-01
FRICAR PAPLICATION NUMBER: 60/089,367
FRICAR PAPLICATION NUMBER: 60/079,624
FRICAR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATCHIN VEY: 2.0
SEQ ID NO 30
LENGTH: 1104
                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Ptilosarcus gurneyi
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Search completed: August 13, 2004, 20:48:16 Job time : 78 secs

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August 13, 2004, 11:19:50 ; Search time 77 Seconds (without alignments) 6061.217 Million cell updates/sec Run on:

US-09-890-463-5 841 1 tccgttatcgctaaacagat......aaaagcggccgctcgaatta 841 Perfect score: Title:

IDENTITY NUC Scoring table: Sequence:

682709 seqs, 277475446 residues Searched:

Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:* Database

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4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
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6: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		øko			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
 	380.4	45.2	678	4	US-09-459-956-6	Sequence 6. Appli
Ω	362.6	43.1	669	4	US-09-459-956-5	'n
m	272.4	32.4	801	4	-459-	
4	198.4	23.6	069	4	-459-	. 2
S	152.6	18.1	969	4	-09-459-956-	'n
9	150.2	17.9	969	4	US-09-459-956-4	
7	131.6	S	720	4	US-09-839-650-1	H
80	126	15.0	1079	4	US-09-609-161B-15	15,
σ	126	S	1079	4	US-09-626-581D-64	64
10	126	15.0	1079	4	US-09-415-765B-64	Sequence 64, Appl
11	126	S	1079	4	US-09-626-580C-64	64,
12	126	15.0	1085	m	US-09-277-716-15	15,
13	122.8	14.6	1021	4	US-09-839-650-2	
14	122.6	14.6	1104	m	US-09-277-716-30	30,
15	122.6	14.6	1104	4	US-09-609-161B-30	30,
16	119.4	14.2	1279	c	US-09-277-716-31	31,
17	119.4	14.2	1279	4	US-09-609-161B-31	31,
	50.8	9.0	368	4	9	53,
Н	50.8	0.9	396	4	09-713-	53,
c 20	50.4	6.0	322	ო	9	216,
c 21	50.4	0.9	322	'n	-09	362
22	49.4	5.9	3275	4	US-09-370-838-151	151,
23	48.4		6412	4	US-09-769-987-1	1, 1
C 24	48	5.7	7218	Н	US-08-232-463-14	
25	47.8	5.7	2030	c,	US-08-706-216-3	3,
26	47.8	5.7	2030	4	US-09-650-284B-3	Sequence 3, Appli
27	46	5.5	1712	4	US-09-148-545-106	Ō.

46 5.5 1822 4 US-09-148-545-105 45.6 5.4 1737 1 US-08-202-056-4 45.6 5.4 1737 1 US-08-284-586-3 45.6 5.4 1737 2 US-08-284-586-3 45.6 5.4 1737 2 US-08-284-586-3 45.6 5.4 1737 2 US-08-801-265-3 45.6 5.4 1737 2 US-08-801-228-3 45.6 5.4 1737 3 US-08-03-228-3 44.6 5.3 144 1 US-08-702-344-26 3 44.4 5.3 1141 4 US-09-312-0138-7 44.4 5.3 1193 4 US-09-312-0138-7 44.4 5.3 1193 4 US-09-336-536-66	Sequence 105, App	Sequence 4, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 114, App	Sequence 7, Appli	Sequence 16632, A	Sequence 26, Appl	78,	Sequence 23, Appl	Sequence 66, Appl							
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	US-09-148-545-105	US-08-202-056-4	US-08-076-093A-3	US-08-701-265-3	US-08-284-586-3	US-08-805-478-3	US-08-802-627A-3	US-08-801-238-3	US-08-801-228-3	US-09-104-296-3	PCT-US94-06380-2	US-08-778-494B-114	US-09-221-013A-7	US-09-621-976-16632	US-08-702-344-26	US-09-800-729-78	US-09-372-422A-23	US-09-336-536-66
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	5.5	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5.3	5.3
8 9 0 1 2 8 4 5 9 7 8 8 9 0 1 2 8 4 5	46	45.6	45.6	45.6	45.6	45.6	45.6	45.6	45.6	45.6	45.6	45.2	45	44.8	44.6	44.4	44.4	44.4
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ALIGNMENTS

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64 TITGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAGGCTG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 TITGAAATAGAAGGCGAAGGAGAGGCCATACGAAGGCCACAATACCGTAAAGCIT 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 AAGGIAACCAAGGGGGGACCTITGCCATTGCTTGGGGATATTTGTCACCACAATTCAG 198
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                                         GENERAL INFORMATION:

APPLICANT: Tsien, Roger Y.

APPLICANT: Tsien, Roger Y.

ITILE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY TITLE OF INVENTION: OPTICAL METHODS

TITLE OF INVENTION: OPTICAL METHODS

FILE REFERENCE: REGEN1290-4

CURRENT FILING DATE: 1999-12-13

PRIOR PILING DATE: 1999-12-03

PRIOR APPLICATION NUMBER: 08/765,860

PRIOR PILING DATE: 1995-06-09

PRIOR PILING DATE: 1995-06-07

PRIOR FILING DATE: 1095-06-06

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                 BY
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Sequence 6, Application US/09459956 Patent No. 6342379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Discosoma sp
US-09-459-956-6
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                                                                         304 GTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGT
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Patent No. 6342379;
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY CURRENT FILING DATE: 1999-12-13;
PRIOR APPLICATION NUMBER: US/09/459,956
PRIOR APPLICATION NUMBER: 08/481,977
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1996-06-06
NUMBER: OF SEQUENCE POTENTIALS DATE: 1996-06-06
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64.0%; Pred. No. 9.2e-67;
iive 0; Mismatches 231;
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FastSEQ for Windows Version 4.0
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Best Local Similarity 64.0
Matches 411; Conservative
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SEQ ID NO 7
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                                                                         GTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTACAAGGTCAAGTTCATTGGC 378
             GTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACCATGTCAAGTTCTCTGGT 363
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APPLICANT: GONZALEZ, III, Jesus E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
TITLE OF INVENTION: OPTICAL METHODS
TITLE OF INVENTION: OPTICAL METHODS
FILE REFERENCE: REGEN1290-4
CURRENT APPLICATION NUMBER: US/09/459,956
CURRENT FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR APPLICATION NUMBER: 08/481,977
PRIOR PELLING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 52
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Pred. No. 4.7e-92;
0; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-459-956-5; Sequence 5, Application US/09459956; Patent No. 6342379
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llarity 73.1%;
Conservative (
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US-09-459-956-5
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Best Local S
Matches 480
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                                                                         AGTCATTCCCGGGGAGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGT
                                                                                                                                                      260 AAGCATTTCCTGACGGAATGTCATATGAAAGGACTTTTTACCTATGAAGATGGAGGAGTTG
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Sequence 3, Application US/09459956

Patent No. 343219

GENERAL INFORMATION:

APPLICANT: Taien, Roger Y.

APPLICANT: Gonzalez, III, Jesus E.

TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS ITILE OF INVENTION: OPTICAL METHODS
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CURRENT APPLICATION NUMBER: US/09/459,956
CURRENT FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR PELING DATE: 1999-05-08
PRIOR PELING DATE: 1995-06-07
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: PCT/US96/09652
PRIOR PILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 3
SEQ ID NO 3
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Best Local Similarity
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US-09-459-956-3
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    ATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGA 314
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GENERAL INFORMATION:
APPLICANT: Genzalez, III, Jesus E.
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
TITLE OF INVENTION: OPTICAL
CURRENT APPLICATION WUMBER: U509/459,956
CURRENT FILING DATE: 1999-05-08
PRIOR FILING DATE: 1999-05-08
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-06
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6342379
GENERAL INFORMATION:
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; ORGANISM: Anemonia majano
US-09-459-956-2
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LENGTH: 690
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JS-09-459-956-2
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GGCTGTCACCAAGGGCGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCA 182
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                                                                                                                    243 ATTCCCGGGGAGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAG----T
                                                                                                                                                GIGTCCTGCTGGATATACATGGGACAGGTCTTTTCTCTTTTGAGGATGGAGCAGTTTGCAT
                                                                                                                                                                              297 GIGTACTGICAGCAATGATTCCAGCATCCAAGGCAACTGITTCATCTACCAIGTCAAGTI
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APPLICANT: Tsien, Roger Y.
APPLICANT: Genzalez, III, Jesus B.
TITLE OF INVENTION: OPTICAL METHODS
FILE REFERENCE: REGEN1290-4
CURRENT APPLICATION OF TRANSMEMBRANE POTENTIALS BY
FILE REFERENCE: REGEN1290-4
CURRENT APPLICATION NUMBER: US/09/459,956
CURRENT APPLICATION NUMBER: US/09/459,956
PRIOR APPLICATION NUMBER: 08/765,860
PRIOR PELING DATE: 1999-05-08
PRIOR APPLICATION NUMBER: 08/481,977
PRIOR APPLICATION NUMBER: PCT/US96/09652
PRIOR APPLICATION NUMBER: 1996-06-06
PRIOR FILING DATE: 1996-06-06
NUMBER: OF SEQ ID NOS: 22
SOFTWARE: FastERO for Windows Version 4.0
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Pred. No. 1.5e-32;
0; Mismatches 233;
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Best Local Similarity 57.5%;
Matches 335; Conservative
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US-09-459-956-4
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US-09-459-956-4
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GENERAL INFORMATION:
APPLICANT: Stratagene
APPLICANT: Stratagene
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APPLICANT: Stratagene
TITLE OF INVENTION: Humanized Polynucleotide Sequence Encoding Renilla Mulleri Green
Patent No. 6645761
TITLE OF INVENTION: Fluorescent Protein
TITLE OF INVENTION: 25436/1755
CURRENT APPLICATION NUMBER: US/09/839,650
CURRENT APPLICATION NUMBER: 2001-04-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 720
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149 AAGGGGGACCATTGCCATTTTCCGAAGACATATTGTCAGCTGGCTTTAAGTACGGAGACA 208
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Patent No. 6645761
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US-09-839-650-1
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AGENERAL INFORMATION:

TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide

TITLE OF INVENTION: Libraries

TITLE OF INVENTION: Libraries

TITLE OF INVENTION: Libraries

FILE REFERENCE: A-66900-3/RMS

CURRENT APPLICATION NUMBER: US/09/626,581D

CURRENT FILING DATE: 1990-10-08

PRIOR FILING DATE: 1990-10-08

PRIOR FILING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin Ver: 2.0

SECTION OF 64
                                                                                                                               356 AGGGTTGCGGCAAAGGGAATATTTTATTCGGCAATCAACTGGTTCAGATTCGTGTCTACA
                                                                                                                                                                                                                                                                                                             416 AAGGGGCCCCACTGCCTTTTGCATTTGATATTGTGTCACCAGCTTTTCAATATGGCAACC
                                                                                                                                                                                                                                                                                                                                                                                               194 TACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGGGA
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                                         GATATACATGGGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATG
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NAME/KEY: CDS
LOCATION: (259)..(975)
OTHER INFORMATION:
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APPLICANT: Broath, Bruce

APPLICANT: Szent-Gyorgyi, Christopher

APPLICANT: PROLUME, IATD:

TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC

TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH

TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS

TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH

TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH

TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH

TITLE OF INVENTION NUMBER: 05/09,161B

PRIOR FILING DATE: 1999-03-26

PRIOR PLING DATE: 1999-10-01

PRIOR PLING DATE: 1998-06-15

PRIOR PLING DATE: 1998-06-15

PRIOR FILING DATE: 1998-06-15

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27

PRIOR PRIOR APPLICATION NUMBER: 60/079,624

PRIOR PRIOR DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27

PRIOR PRIOR DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-27

PRIOR PRIOR PRIOR DATE: 1998-03-27

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CTTCACCAAGTACCCCAACGACATCAGCGACTACTTCATCCAGAGCTTCCCCGCCGGCTT 284
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. OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP)
US-09-609-161B-15
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ilarity 50.0%; Pred. No. 1.1e-25;
Conservative 0; Mismatches 315;
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Patent No. 6436682
GENERAL INPORMATION:
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ORGANISM: Renilla mulleri
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US-09-609-161B-15
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ORGANISM: Renilla muelleri
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; OTHER INFORMATION:
US-09-626-580C-64
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                                                                                                                       134 AGGCCGACCTCTGCCATTTGCTTGGGATATTTTATCACCACAGTGTCAGTACGGAAGCA 193
                                                                                                                                                                                                                                               GATATACATGGGAGAGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATG 313
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Sequence 64, Application US/09415765B

Patent No. 6548632

GENERAL INFORMATION:
APPLICANT: Anderson, David
ITILE OF INVENTION: Libraries
ITILE OF INVENTION: Libraries
ITILE OF PREFERRICE: A66900-1/RMS/AMS
CURRENT APPLICATION NUMBER: US/09/415,765B

CURRENT FILING DATE: 1999-10-08

PRIOR PLILING DATE: 1999-10-08

PRIOR PLILING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                  194 TACCATTCACCAAGTACCCTGAAGACATCCCTGACTATGTAAAGCAGTCATTCCCGGGGA
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AACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCG
                            296 AAGTAATGTCGTATAAAGTAAATCTGGAAGGAATTGTAAACAACCATGTTTTTACAATGG
                                                             416 AAGGGGCCCCACTGCCTTTTGCATTTGATATTGTCACCAGCTTTTCAATATGGCAACC
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ORGANISM: Renilla muelleri
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LOCATION: (259
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LENGTH: 1079
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Anderson, David

APPLICANT: Anderson, David

APPLICANT: Bogenberger, Jakob M.

APPLICANT: Beele, Beau R.

APPLICANT: Peele, Beau R.

TITLE OF INVENTION: PUSSIONS OF SCAFFOLD PROTEINS WITH RANDOM PEPTIDE LIBRARIES

FILE REFERENCE: A-66900-2/RMS/AMS

CURRENT FILING DATE: 2000-07-27

FRIOR APPLICATION NUMBER: US 09/415,765

PRIOR FILING DATE: 1999-10-08

PRIOR FILING DATE: 1999-10-08

PRIOR FILING DATE: 1999-10-08
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   14 AACAGATGACCTACAAAGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCG
                                                               296 AAGTAATGTCGTATAAAGTAAATCTGGAAGGAATTGTAAACAACCATGTTTTTACAATGG
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Patent No. 6562617
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SOFWARE: PatentIn version 3.1
SEQ ID NO 60
LENGTH: 1079
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Gaps

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355 133

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313

193

595 373 655 715

493

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GENERAL INFORMATION:
APPLICANT: Strategene
TITLE OF INVENTION: Humanized Polynucleotide Sequence Encoding Renilla Mulleri Green
Patent No. 6645761
TITLE OF INVENTION: Fluorescent Protein
TITLE OF INVENTION: Fluorescent Protein
FILE REPERENCE: 25436/1755
CURRENT APPLICATION NUMBER: US/09/839,650
CURRENT FILING DATE: 2001-04-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
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                                                   ; FEATURE:
; OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP)
US-09-277-716-15
                                                                                                                                           Score 126; DB 3; Length 1085.
Pred. No. 1.1e-25;
0; Mismatches 315; Indels
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                                                                                                                                        Query Match
Best Local Similarity 50.0%;
Matches 315; Conservative 0
       NAME/KEY: CDS
LOCATION: (259)..(975)
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                                                 Gaps
                                                 0;
    Length 1079;
Score 126; DB 4; Length 10
Pred. No. 1.1e-25;
0; Mismatches 315; Indels
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APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
CURRENT PROLUCATION: LUCIFERASES, FLUORESCENT
CURRENT FILING DATE: 1999-03-26
BARLIER APPLICATION NUMBER: 60/102,939
BARLIER FILING DATE: 1998-10-01
BARLIER FILING DATE: 1998-10-01
BARLIER FILING DATE: 1998-06-15
BARLIER PLICATION NUMBER: 60/089,367
BARLIER FILING DATE: 1998-06-15
BARLIER PILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
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GENERAL INFORMATION:
15.0%;
                     al Similarity 50.0
315; Conservative
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LENGTH: 1079
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435 438 498 555 558 615 618

us-09-890-463-5.rni

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APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: STOLUME, LTD.
APPLICANT: PROLUME, LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIG
TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
FILE REFERENCE: 24729-121B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 ACATGGGAGAGAGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGATTCC 318
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                                                                                                                                                                         OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) -09-277-716-30
                                                                                                                                                                                                                                     Length 1104;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                     Score 122.6; DB 3;
Pred. No. 9.7e-25;
0; Mismatches 314;
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Best Local Similarity 49.8%;
Matches 311; Conservative
                                                                             gurneyi
                                                      TYPE: DNA
ORGANISM: Prilosarcus g
FBATURE:
NAME/KEY: CDS
LOCATION: (34)..(747)
Ver.
SOFTWARE: Patentin
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US-09-609-161B-30
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                  SEQ ID NO 30
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APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LID
TITLE GF INVENTION: LUCIPERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
CURRENT APPLICATION NUMBER: 05/02/339
EARLIER APPLICATION NUMBER: 60/102,939
EARLIER PILING DATE: 1998-10.
EARLIER PILING DATE: 1998-06-15
EARLIER PILING DATE: 1998-06-15
EARLIER PILING DATE: 1998-06-15
EARLIER PILING DATE: 1998-06-15
EARLIER PILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
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                                                                                                                                                            Gaps
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                                                                                                                    Length 1021;
                                                                                                                  Score 122.8; DB 4; Length Pred. No. 8.2e-25; 0; Mismatches 317; Indels
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GENERAL INFORMATION:
                                                                                                                tcn 14.6%;
al Similarity 49.7%;
313; Conservative
  ORGANISM: Renilla muelleri
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                                       NAME/KEY: exon
LOCATION: (259)..(976)
-09-839-650-2
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US-09-277-716-30
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1 LOCATION: (34)..(747)
2 OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (insert A)
US-03-609-161B-30
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Best Local Similarity 49.8%; Pred. No. 9.7e-25;
Matches 311; Conservative 0; Mismatches 314; Indels 0;
CURRENT APPLICATION NUMBER: US/09/609,161B
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/277,716
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-10-01
PRIOR FILING DATE: 1998-10-01
PRIOR FILING DATE: 1998-10-01
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-06-15
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
SOFTWARE: PATCH NOWER: 60/079,624
PRIOR FILING DATE: 1998-03-27
SOFTWARE: PATCH NOS: 32
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Search completed: August 13, 2004, 20:48:15 Job time : 79 secs

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Pigm	BD248905 Pigment p	Arsasisa Goniopora Ax699793 Semience	AX699755 Sequence	AX699783 Sequence	AX699753 Sequence	AX699765 Sequence	AX699923 Sequence	AX699759 Sequence	AX699921 Sequence	AX699927 Sequence AX699933 Sequence	AX699781 Sequence	AX699929 Sequence	AX699871 Sequence	AX699925 Sequence	AX699827 Sequence	AX699829 Sequence AX699819 Sequence	AX699821 Sequence		S	AX699771 Sequence AX699773 Sequence	S	AX699803 Sequence	AX699817 Sequence .	AX699835 Sequence	AX699847 Sequence	AX699779 Sequence	AX699899 Sequence	AX699833 Sequence	AX699879 Sequence	AX699805 Segmence	S	AX699813 Sequence AX699769 Sequence	va		3/2	10C1 10C1	DNA linear PAT 17-JUL-2003			Onthords. Scantharia. Scleractinia.	a.	e - 2002:
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į	Kesuit No. Scor	1 8	o r	~ (¢	φ	648	647	647	647	645	2 642	640	5 639	6 639	7 637 8 637	9 637	0 636	2 636	969 6	5 633	6 631	631	9 631	0 631	2 631	3 629	5 629	6 629	7 628	9 628	0 628	9 49	9	44 62 45 627.				RESULT 1 BD248906			KEYWORDS C	ORGANISM		AUTHORS TITLE JOURNAL

840

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PAT 17-JUL-2003
561 IGCCGTTTTTCAGAGTCAAATCAAGGCACAAATACGCAGTGGCGTAAAAAACGTAGATT 720
                                                                                                                                                                        Bukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Scleractinia, Astrocoeniina, Acroporidae, Acropora.

1 (bases 1 to 841)
Guldberg,O.H. and Dove,S.
Pigment protein from coral tissue
Patent: JP 2002535978-A 1 29-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OVE HORGH GULDBERG, SOPHIE DOVE
C12N15/09, A61K7/42, C07K14/435, C09B61/00, C09K11/06, C12N1/15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N21/78, C12N15/00, C12N5/
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                                                CTGATTTTAGCTTATAGAAGTAGGAACGAAGAAGTGTAAAACAACCATTAATGATTAAACT
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Pred. No. 6e-194;
1; Mismatches 10; Indels 0;
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Key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:140238"
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al tissue.
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JP 2002535978-A/1
29-OCT 2002
02-FEB-2000 JP 2000597303
02-FEB-1999 AU PP 8463
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BD248905.1 GI:33058675
JP 2002535978-A/1.
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98.7%;
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Best Local Similarity 98.7
Matches 830; Conservative
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DEFINITION
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AUTHORS
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JOURNAL
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    .841
/organism='Acropora aspera (plate coral)'

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100.0%; Pred. No. 5.1e-198;
ive 0; Mismatches 0;
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Key Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:140238"
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(Dases 1 to 881)

Gurskaya,N.G., Fradkov,A.F., Terskikh,A., Matz,M.V., Labas,Y.A., Martynov,V.I., Yanushevitch,Y.G., Lukyanov,K.A. and Lukyanov,S.A.

FEBS Lett. 507 (1), 16-20 (2001)
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Location/Qualifiers
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/organism="Goniopora tenuidens"
/mol_type="mRNA"
/db_xref="taxon:75301"
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KOGPLDFPANDILSPQSQYGSIPFTKPFDIPDYVKQFPPEGTVTWERINMFKDGAVCTV
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KLEGGGHYLCEFKSTYKAKKPVMMFGYHYVDRKLDVTNHNKDYTSVEQCEISIARKPV
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Porites murrayensis
Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia, Scleractinia,
                                                                                                                                                               Karan,M., Brugliera,F., Mason,J., Jones,B.L., Dove,S.G.,
Hoegh-Guldberg,I.O. and Prescott,M.
Hoell visual characteristic-modifying sequences
Patent: WO 02070703-A 61 12-SEP-2002,
NUFARM AUSTRALIA LIMITED (AU); The University of Queensland (AU)
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Pred. No. 1.5e-152;
); Mismatches 22;
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                                                                     AX699793.1 GI:29500268
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/note="unnamed protein product"
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KLEGGGGHYLCEFKSTYKAKKPVRMFGYHYVDRKLDVTNHNKDYTSVEQCEISIARREPV
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Hoegh-Guldberg,I.O. and Prescott,M.
Cell visual characteristic-modifying sequences
Patent: WO 02070703-A 23 12-SEP-2002;
NUFARM AUSTRALIA LIMIED (AU); The University of Queensland (AU)
Location/Qualifiers
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Pred. No. 3.3e-151;
0; Mismatches 6;
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Astrocoeniina, Acroporidae, Acropora.
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Sequence 23 from Patent WO02070703.
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SNDSSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEPNTERLLARDGMLIGNNFMAL
             TACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGGAGCAGACGGTAAGG
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AX699753
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/translation="SYIAKOMTYKYYMSGTVMGHYFEVEGDGKGKPYEGEGTVRLTVT
KGPLDFAMDLLSPQSQYGSIPFTKYPEDIPDYVKQSFPEGTYWERIMNFEDGAVCTV
SNDSSIQGNCFIYHVKFGSLMPFPROPWDGKKTQGREPHTELLFARDGMLIGNNFMAL
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Hoegh-Guldberg,I.O. and Prescott,M.
Cell visual characteristic—modifying sequences
Patent: WO 02070703-A 51 12-SEP-2002;
Patent: WO LONGOOD A 51 LOUITED (AU); The University of Queensland Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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AX699783.1 GI:29500258
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Hoegh-Guldberg,L.O. and Prescott,M.
Hoegh sual characteristic—modifying sequences
Patent: WO 02070703-A 21 12-SEP-2002,
NUFARM AUSTRALIA LIMITED (AU); The University of Queensland (AU)
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Sequence 53 from Patent W002070703.
AX699785.1 GI:29500260
  type="unassigned DNA"
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        "ot_ref="taxon:46696"
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/note="unnamed
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Hoegh-Guldberg,I.O. and Prescott,M.
Gell visual characteristic-modifying sequences
Patent: WO 02070703-A 31 12-285P-2002,
NUFARM AUSTRALIA LIMITED (AU); The University of
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                                          Score 647.2; DB 6;
Pred. No. 6.5e-150;
0; Mismatches 8;
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                                                    Similarity 98.652; Conservative
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KLEGGGHYLCEFKSTYKARKPVKMPGYHYUDRKLDVTNHNKDYTSVEQREISIARKPV
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Pred. No. 6.5e-150;
0; Mismatches 8;
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PAT 02-APR-2003

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TCATTCCCGGAGGATATACATGGGAGAGCATCATGAACTTTGAAGATGGTGCAGTGTGT
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Eukaryota, Metazoa, Cnidaria, Anthozoa, Zoantharia,
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Hoegh-Guldberg,I.O. and Prescott,M.
Gell visual characteristic.modifying sequences
Patene: WO 02070703-A 191 12-SEP-2002,
NUFARM AUSTRALIA LIMITED (AU); The University of
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    .669
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KLAGGGHYLCEFKSTYKARKFVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKFV
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                                   Dove, S.G
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                                Karan, M., Brugliera, F., Mason, J., Jones, E.L., D
Hoegh-Guldberg, I.O. and Prescott, M.
Cell visual characteristic-modifying sequences
Patent: WO 02070703-A 53 12-SEP-2002;
NUFARM AUSTRALIA LIMITED (AU); The University
                                                                                                                                                                             /mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Millepora sp. (Hydrozoan)"
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/note="unnamed protein product"
/codon_start=1
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Matches 652; Conservative
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                 AAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAGGAAG
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Hoegh-Guldberg,J.O. and Prescott,M.
Cell visual characteristic-modifying sequences
Patent: WO 02707003-A 189 12-SEP-2002;
NUFARM AUSTRALIA LIMITED (AU); The University of Queens
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Pred. No. 1e-148;
0; Mismatches 1
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    .669
    /organism="Acropora aspera"
/mol_type="unassigned DNA"
/db_xref="taxon:140238"

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SNDSSIQGNCFIYHVKFSGLMFPPNGPVMQKKTQGWEDNTERLSARDGMLIGNNFMAL
KLEGGGHYLCEFKSTYKARKFVKMFGYHCVDRKLDVTNHNKDYTSVEQREISIARKPV
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Faviina, Mussidae, Acanthastrea.
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                                                                                                                                                                                                          Dove, S.G.
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Hoegh-Guldberg, I.O. and Prescott, M.
Cell visual characteristic-modifying sequences
Patent: WO 0207003-A 27 12-SEP-2002;
NUFARM AUSTRALIA LIMITED (AU); The University of
Location/Qualifiers
                                                       linear
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Pred. No. 1.6e-149;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                       /organism="Acanthastrea echinata"
/mol_type="unassigned DNA"
/db_xref="taxon:51051"
                                                                                                                                                                                                                                                                                                                                                     <1. ... >660
/note="unnamed protein product"
                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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/b_xref="G1:29500235"
/db_xref="RRWTREMB1:CAD87448"
                                                       660 bp | 27 from Patent W002070703.
                                                                                                AX699759.1 GI:29500234
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                   AAGTTAGAAGGAGGTCGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
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481 AAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG
                                                                                                          544 cerergaagargecaaggararcaerargrigaecgcaaaerggargraaccaarcaaae
                                                                                                                                                 AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
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                                                                          CCTGTGAAGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
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98.2%; Pred. No. 2.5e-148;
tive 0; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unidentified"
/mol type="unassigned DNA"
/db xref="taxon:32644"
/note="Tubastrea sp."
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 AAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAG 540
                     AAGTTAGAAGGAGGTGGTCATTTGTGTGAATTCAAATCTACTACAAGGCAAAGAAG 543
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                                                                          CCTGTGAAGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
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                                                                                                            544 CCTGTGAAGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAATCACAAC
                                                                                                                                                   AAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCC
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Hoegh-Guldberg,I.O. and Prescott,M.
Cell visual characteristic-modifying sequences
Patent: WO 2070703-A 195 12-SEP-2002;
NUFARM AUSTRALIA LIMITED (AU); The University of Queen
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 669;
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98.2%; Pred. No. 2.5e-148;
iive 0; Mismatches 12;
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/note="Tubastrea sp."
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Sequence 195 from Patent WO02070703
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/translation="SVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYECEQTVKLTVTKGPLPFAWDILSPOSQYGSIPFTKYPEDIPDYVKQSFPEGYTWERINNFEDGAVCTVSNDSIQGNCFIYHVKFSGLNFPPNGPVMQKKTQGWEDNTERLFARDGMLIGNNFMALKLEGGGGHYLCEFKSTYKARKFVKMPGYHYVDRKLDVTNHNKDYTSVEQREISIARKFVVA
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Hoegh-Guldberg,I.O. and Prescott,M.
Cell visual characteristic-modifying sequences
Patent: WO 02070703-A 49 12-SEP-2002;
NUFARM AUSTRALIA LIMITED (AU); The University of Queensland (AU)
Location/Qualifiers
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 AAGTTAGAAGGAGGTGGTCACTATTTGTGTGAATTCAAATCTTACAAGGCAAAGAAG
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.larity 98.0%; Pred. No. 6.3e-148;
Conservative 0; Mismatches 13;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                 OM nucleic - nucleic search, using sw model
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                               Run on:
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TITLE JOURNA	COMMENT				_	
	Description	CK159216 FGAS04062	CF805258 lad65f03.	BU563278 AGENCOURT	AL220324 Tetraodon	
SUMMARIES		9	CF805258	BU563278	CNS02YZV	
	DB	14	14	13	59	
	ength	998	297	820	667	
مدن	Query Match Length DB ID	6.8	6.7	6.7	9.9	
	Score	57	56.	26	55.6	
į	ult No.	П	7	٣	4	
1	Resul No	υ			υ	

AL066995 Drosophil	60292		71722				BX40348	59 FGAS03	Æ	AL077453 Drosophil		3 tz43c1		CF309143 ABF03-D	AL663605 AL663605		BI746239 rm24f05.y					CK194319 FGAS00274				$^{\circ}$		BG662904 DKA05B01	CF328004 NACL02-						202	3218 sh54a0	BI378622 BFLG1 000		5086	S		mRNA linear EST 05-DEC-2003
CNS007CK	BI527017	BX398622	CD771722	CB958074	BU56709B	BQ566832	BX403488	CK155159	AL558886	CNS00KB5	AI796743	BE047863	AU033588	CF309143	AL663605	CK197676	BI746239	CK196558	CK240710	CA324119	BUS55445	CK194319	CF423560	BX403935	BG609931	BF294370	AU262401	BG662904	CF328004	CD641692	CK195879	BU946204	CK151995	BX328575	BX446507	AW433218	BI378622	BM985610	5208	ALIGNMENTS		866 bp
29	12	13	14	14	13	13		4			6	10			6	14	12	14	14	14	13	14	14	13	12	10	σ;	77	4.4	4 0	, L	13	14	13	13	10	12	12	14			£
359	683	1201	635	362	752	278	539	872	918	1101	242	314	330	418	722	794	399	855	249	528	901	852	278	1201	278	417	422	441	561	0 0	000	888	851	937	1184	223	521	812	898			
6.5	•	6.5	6.5	•	•	•	6.5						٠,			6.4	6.4		•	•	•			•			•	•	•	•	יי פ			6.3	•	6.2		•	•			CK159216 FGAS040623
55	22	22	4.	4.	4.	4.	4	4	4	54.2	m	m	(1)	53.8	53.8	m	3	3	53.4	3	3	m	23	53	52.8	52.8				0.70	0.7 0.0		52.6	52.6	52.6	52.4	52.4	52.4	52.4			-
Ŋ	9	c 7	80	σ	10	11	c 12		14	15	c 16		18	19		c 21	22	c 23	24	25	26	c 27	28	c 29	30	31	35		3.4		3.45			c 40	4	42	43	44	c 45		RESULT 1 CK159216/c	LOCUS

CK159216/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	CK159216 866 bp mRNA linear EST 05-DEC-2003 FGAS040623 Triticum aestivum CDNA, mRNA sequence. CK159216 CK159216 CK159216.1 GI:38985155 EST. Triticum aestivum (bread wheat)
ORGANISM	Triticum aestivum Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae, Triticeae, Triticum.
REFERENCE AUTHORS	<pre>1 (bases 1 to 866) Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D., Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A., Links,M.G., McGarthy,E.L., Monroy,A., Muzak,I., Nilson,D., Penniket,C., Roach,J.L. and Sarhan,F.</pre>
TITLE JOURNAL COMMENT	Functional Genomics of Abiotic Stress In Wheat and Canola Crops Unpublished (2003) Contact: Wm L Grosby Bloinformatics
	University of Saskatchewan, Department of Computer Science 10:101 Engineering Building, 57 Campus Drive, Saskatoon, Saskatchewan, S7N 5A9, Canada Tel: 306 966 1769 Fax: 306 966 2033

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Conservative
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Matches 98; Conserv
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S Tidwell,R. Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,B., Bennet,J., Watie,T., Tagareishvili,R., Belaygorod,L., Grow,A., Maguire,L., Watherton,R. and Wilson,R.
Waterston,R. and Wilson,R.
Washu Stem cell EST Project
L Unpublished (2002)
Contact: Jeff Gordon and Mike Lovett
Unpublished (2002)
Contact: Jeff Gordon and Mike Lovett
Washu Human Genetics Division
Washuy Human Genetics Division
Washington University School of Medicine
1st strand of cDNA was synthesized with reverse transcriptase and oligo(dY) beads, then cDNA was amplified by PCR using modified SMART primers. The final CDNA was amplified by PCR using modified SMART primers. The Hinal CDNA was cloned in pAMPI vector in annealing reaction with Uracil DNA dycosylase (UDG). Library constructed by X.Korshunova and M. Lovett. Library materials provided by Mills UC & Gordon JI.
Putative full length read
                      This sequence is the direct result of the Base calling software phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [124,60].

Plate: Talt538 row: B column: 11.
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                                                                                                                                                                                                                                                                                                                    /db xref="taxon:4565"
/lab host="DH5 alpha"
/clone lib="Triticum aestivum FGAS: TaLt5"
/note="Organ: Crown; Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype P1178383 cold hardened at 2 C for 21 days and 49 days P1178383 cold hardened at 2 C for 21 days and 49 days fequal amount of cDNA pooled together before subtraction, tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H) (driver). Modified Smart cDNA (Clontech) priming and non-directional cloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  673 AGAGTCAAATCAAGGCACAAATACGCAGAGTGGCGTAAAAAAGGTAGATTCTGATTTTAGCT 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 AAAATAAAAACAAAAATTTTGGTTTTAAGCAAAAAAAGGGGTTTTTAATTTTTGTA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 AAAAAAAAAAACTGGGAAAATAAAAAAATTAAAACACGGAATTTTTTAAAAA 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.8%; Score 57; DB 14; Length 866;
60.8%; Pred. No. 7.5;
live 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="Wheat line PI 178383"
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Seq primer: -40RP from Gibco.
Location/Qualifiers
Email: fgas ests@cs.usask.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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CF805258.1 GI:37974718
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Best Local Similarity 60.8
Matches 93; Conservative
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EST 16-SEP-2002
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Gastric Epithelial Progenitor 2"
/note="Vector: pAMP1; lst strand of cDNA was synthesized
with reverse transcriptase and oligo(dT) beads, then cDNA
was amplified by PCR using modified SMART primers. The
final cDNA was cloned in pAMP1 vector in annealing
reaction with Uracil DNA Glycosylase (UDG). Library
constructed by Y. Korshumova and M. Lovett. Library
materials provided by Mills UC & Gordon JI."
                                                                                                                                                                             /tissue_type="Laser-captured isthmal cells from tox176 transgenic mice"
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Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.b column: 15
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MARNOCINET 10248984 WIH MGC 143 Mus musculus cDNA clone
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                                                         /mol_type="mRNA"
/db xref="taxon:10090"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
/lab_host="DH5alpha"
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Mus musculus
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VERSION
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CNS007CK
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adaptors were used in cloning as follows:
5. AAGCAGTGATCAACGCAAGAGGGCATGGG-3, and
5. ATTCTAAAGGCGAGGCGCAAAGGT(30)NN-3. Full-length
enriched library was constructed using the Clontech
Creator SWART kit and size-selected to contain the 0.2-0.5
kb size fraction (other fractions present in NIH MGC_144).
Library created in the laboratory of M. Brownstein (NIMH,
NIH). Note: this is a NIH_MGC Library."
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Terracdon nigroviridis genome. For more information, please take a look at
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                       39 ACTGCTCTTCTGAAGGTCCTGAGTTCAATTCCCAGCAACCACATGGTGGTCACAACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                       670 TTCAGAGTCAAATCAAGGCACAAATACGCAGTGGCGTAAAAAACGTAGATTCTGATTTTA
                                                                                                                                                                                                                                                                                                                              610 ACTICCGTIGAGCAGIGIGAAAITICCAFIGCACGCAAACCIGIGGICGCCIGCCGTTTI
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                                                                                                                                                                                                                                  6.7%; Score 56; DB 13; Length 82
53.7%; Pred. No. 11;
ive 0; Mismatches 100; Indels
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Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Googawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pland BAC libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACRAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR15J06 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                      678 CAAATCAAGGCACAAATACGCAGTGGCGTAAAAAACGTAGATTCTGATTTTAGCTTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 AAGTAGGAACGAAGAAGTGTAAACAACCATTAATGATTAAACTTTTTGAAAACAACGCCAT
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              24; Mismatches
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                                                                                                                                                                                                                                                                                                                                      6.6%; Score 55.6; 48.1%; Pred. No. 14
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/db xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fly), genomic survey sequence.
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/clone_lib="RPCI-98"
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hes 76; Conservative
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us-09-890-463-6.rst

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BX398622 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI061YJ01 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contract: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVNY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO6ICED1QPI.
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AGENCOURT 14738271 NIH MGC 190 Mus musculus cDNA clone
IMAGE:30501368 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              679 AAATCAAGGCACAAATACGCAGTGGCGTAAAAAACGTAGATTCTGATTTTAGCTTATAGA 738
/clone="CSODIOGIVO1"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u> ААААААСССАКАААААААВААВАААААААААААМААТАТWWTTTTTWWWWTTWWWATW</u> 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            739 AGTAGGAACGAAGAGTGTAAACAACCATTAATGATTAAACTTTTGAAAACAACGCCATA 798
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Li, Was, Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                             DB 13; Length 1201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.5%; Score 55; DB:
43.5%; Pred. No. 13;
rative 34; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BX398622.1 GI:30617636
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 683)
S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

I (npublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
COND Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Http://mage.llnl.gov
Plate: LLAMI1161 row: m column: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
site_2: Noti; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAAAAACGTAGATTCTGATTTTAGCTTATAGAAGTAGGAACGAAGAGTGTAAACAACC 765
                                                                                                                                                                                GTAACCAATCACAACAAGGATTACACTTCCGTTGAGCAGTGTGAAATTTCCATTGCACGC
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                                                                                                  107 AAAAAACGTAGATTCTGATTTTAGCTTATAGAAGTAGGAACGAAGAAGTGTAAACAACCA
                                                                                                                                        646 AAACCTGTGGCCTGCCGTTTTTTCAGAGTCAAATCAAAGCACAAATACGCAGTGGCG
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18;
                       Length 359;
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51.9%; Pred. No. 18;
ive 0; Mismatches 115; Indels
                                                            Indels
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/clone="IMAGE:5059775"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
                                                            38;
                     29;
                       DB
                                                          7; Mismatches
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High quality sequence stop: 437.
Location/Qualifiers
                     Score 55;
Pred. No.
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BI527017.1 GI:15351809
                     6.5%;
                                                            Conservative
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Matches 124; Conserv
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Best Local !
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Non-normalized full-length enriched library 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCCATTATGCCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGAGGGGCGACATG-dT(30) BN-3' (where B = A,
c, or G and N = A, C, G, or T). Average insert size 1.71
kb (range 0.5-3.0 kb). 15/15 colonies contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by clontech Laboratories (Palo Alto, CA)
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                                                                                               Contact: Daniels S. Gerhard, Ph.D.
Contact: Daniels S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg: 31 Rm10A07 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Yoshihiko Yamada, Takashi Nakamura, NIDCR
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM223 row: o column: 09
High quality sequence stop: 305.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/dD_xref="taxon:10090"
/dD_xref="INAGE:30501368"
/lab_host="NHGB:30501368"
/clone_lib="NHH MGC_190"
/clone_lib="NHH MGC_190"
/note="Organ: Pooled - Molar; Vector: pDNR-LIB; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               610 ACTICCGITGAGCAGIGIGAAAITICCATIGCACGCAAACCIGIGGICGCCIGCCGTITI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 570 TTCAGAGTCAAATCAAGGCACAAATACGCAGTGGCGTAAAAAACGTAGATTCTGATTTTA
                   1 (bases 1 to 635)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 20;
0; Mismatches 102; Indels 0;
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/organism="Mus musculus"
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                                                                                  Unpublished (1999)
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Best Local Similarity 53.2
Matches 116; Conservative
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CB958074
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Sill (ggocattatgoca): Site 2: Sill (ggocacttagoca): Juleary is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyoid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGACGATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCGCCGATTGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCGCCGATTGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCGCGCATG-GT(30) BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: NDCM148 row: c column: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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/db xref="taxon.9606"
/db xref="taxon.9606"
/lab host="IMAGE:30351140"
/clone lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 752)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.5%; Score 54.6; I
59.2%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 337.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU567098.1 GI:22917398
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Matches 93; Conserv
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source
                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="mixed (pool of 40 RNAs)"
/lab host="nDHOB (T1-phage-resistant)"
/clone_lib="NIH MGC_l41"
/note="Vector: pDNH-LiB; Site_1: Sfil (ggccattatggcc);
Site_2: Sfil (ggccgcctcggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder-2%, blocd 13.4%, brain -5.6%, breast - 12.5%, colon -4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5'-ATTCTAGAGGCCGAGGCGCCAATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech creator SWART kit and size-selected to contain the 0.2-0.5 kb size fraction (other fractions present in NIH MGC 142). Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 19-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ566832 278 bp mRNA linear EST 19-JUN-2005 gi70h11.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi70h11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 278)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      669 TITCAGAGTCAAATCAAGGCACAAATACGCAGTGGCGTAAAAAACGTAGATTCTGATTTT
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CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCMS52 row: k column: 20
High quality sequence stop: 400.
Location/Qualifiers
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59.2%; Pred. No. 19;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                              'organism="Homo sapiens"
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/clone="IMAGE:6606668"
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                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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BQS66832.1 GI:21470149
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Unpublished (2002)
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Matches 93; Conservative
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                        FEATURES
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to manutacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector Xit (catalog # 237211, Stratagene) and Uni-Zap XR digapack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, WSA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo (dT) linker-primer that contains an Xho I site. Pites strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (WMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DAP polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR adapters in the presence of ligase and digested with Xho I. The CDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clonteen Chroma Spin-1000 (Clonteen, Palo Alto, CA) columns to enrich for CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and upon tirration on XLI Blue NRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescue plasmid DNA from the phages. Upon plating of the rescue plasmid DNA from the phages. Upon plating of concertes (FM) plasmid purification kit (Invitrogen, Concerte (FM) plasmid purification kit (Invitrogen, Carlsbad, A3 as instructed by the manufacturer. EST from the 5' end of the CDNA perseparent and 25% at reacret had or secuence of the manufacturer. EST from the 5' end of the CDNA secuencing chemistry (Adopled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blosystems, Foster City, Ch. Sequencing reactions were performed on MJ Tetrad thermal cyclers (MR Research, Waltham, MA), and analyzed on 3700 automated capillary sequences using POP5 polymer (Applied Blosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have i copy, 14.3% 2, 12% 3.10; 1.4% 11.50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev state="most canal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cervical dislocation followed by decapitation, the bulla was removed and opened in leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiculus. Total RNA was extracted using the micro Fasttrack kit (catalog # Kip33-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions Reverse transcription and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA) Command.
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
                                                                                                                                       Email: Kacharb@nidcd.nih.gov
Plate: 70 row: h column: 11
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="BALB/c"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 539)
                                                                                                                                                                                                        610 ACTICCGTIGAGCAGTGTGAAATTTCCATTGCACGCAAACCTGTGGTCGCCTGCCGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 ccataacgagarctgargccrcrrcrgcrgcgrcrgagagacarcracagrarrana
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                                                                                                                                                                                                                                                                                                                                                                                                                670 ITCAGAGTCAAATCAAGGCACAAATACGCAGTGGCGTAAAAAACGTAGATTCTGATTTTA
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7316.r
Contact: France Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBA002ZE10FP1.
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     6.5%; Score 54.4; DB 13;
53.2%; Pred. No. 34;
tive 0; Mismatches 101;
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/mol type="mRNA"
/cultivat="Wheat line CI 14106"
/db xref="Laxon:4565"
/lab host="BHS alpha"
/clone lib="Triticum aestivum FGAS: TaLt2"
/clone lib="Triticum"
/clone genotype CI14106 cold hardened at 2 C for I day (24 H) (tester) and subtracted against genotype Norsterar cold hardened at 2 C for 21 days and 49 days (equal amount of cDNA pooled together before subtraction, driver) . Nitro-pyrole anchored oligo-dT priming and non-directional cloning."
                                                                                                                                                                                                                                                                                                                                              CK155159 872 bp mRNA linear EST 05-DEC-2003 FGAS033880 Triticum aestivum FGAS: TaLt2 Triticum aestivum cDNA,
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Functional Genomics of Abiotic Stress In Wheat and Canola Crops
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Contact: Wm L Crosby
Bioinformatics
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                                                         41558886 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens cDNA clone CSODJ015YHO6 5-PRIME, mRNA sequence.
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Was incrmalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
http://www.genoscope.ns.fr/
cg1-bin/cluster.cg1?seq-CSODG015DD03QP1&cluster-6274.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODG015DD03QP1.
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/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
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                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR39POS of RPCI-98 library from Drosophila melanogaster (fruit
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Ompublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12903846.
Contact: Genoscope
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/clone="CS0DJ015YH06"
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by 191000 by Man. Carried out as part of a Determination of this BAC-end sequence was carried out as part of a Collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegaw and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 19;
8; Mismatches
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/db_xref="taxon.7227"
/clone="backs9P05"
/clone lib="RPCI-98"
/note="end : T7"
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